

Search Results -

Search Results -				
Term	Documents			
	474			
TTR.USPT.	14			
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US Patents Full-Text Database

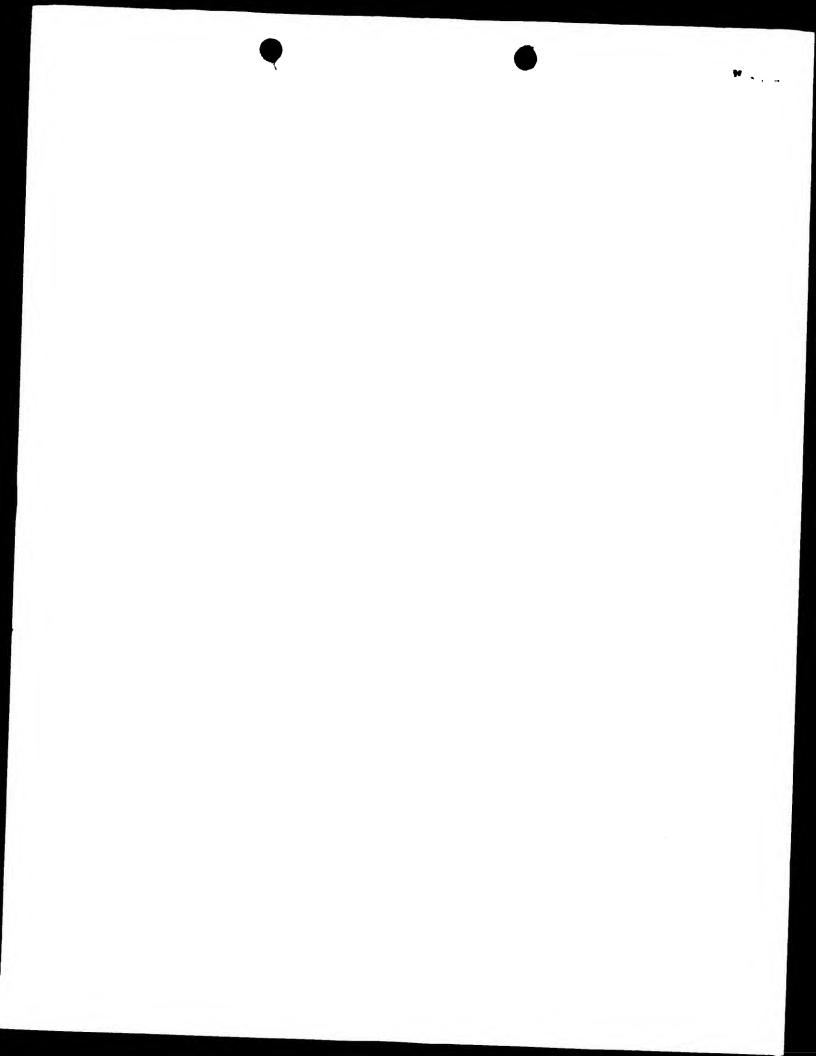
US Pre-Grant Publication Full-Text Database JPO Abstracts Database

EPO Abstracts Database

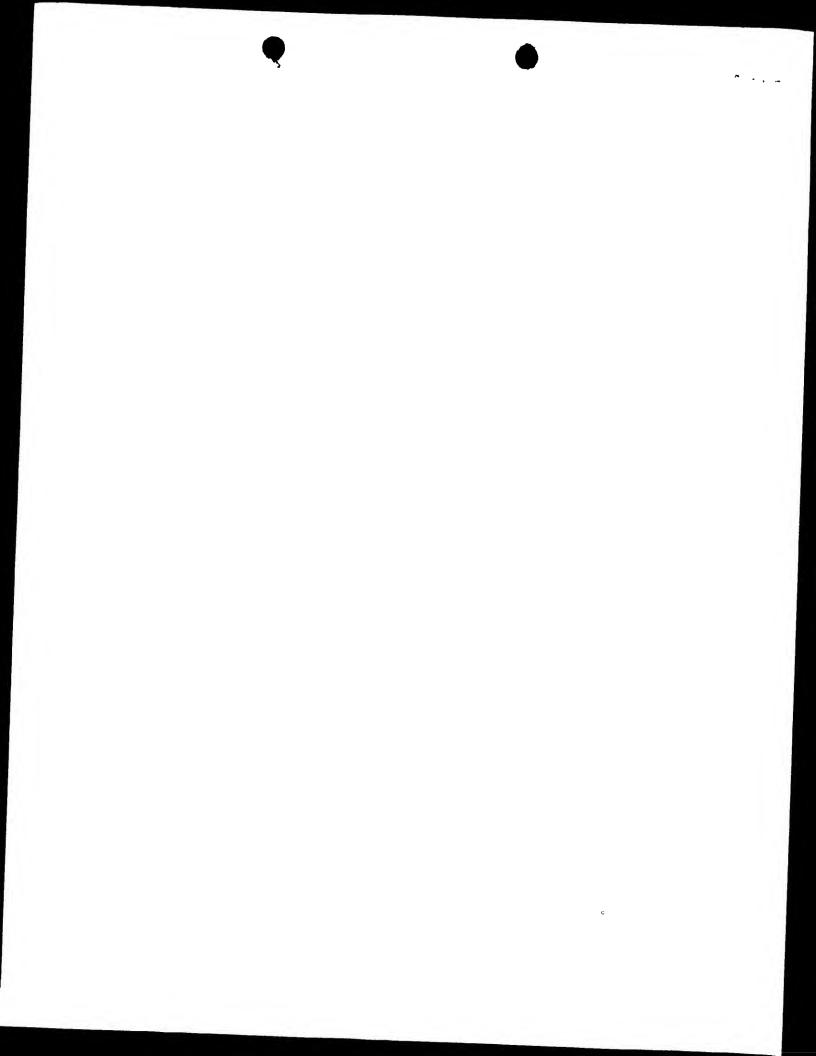
Derwent World Patents Index Database: IBM Technical Disclosure Bulletins

Refine Search:	promoter	Clear
	Search History	

Today's Date: 1/9/2002



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DD Name	Query	Hit Count S	
DB Name	11 and ttr promoter	2	<u>L13</u>
USPT		0	<u>L12</u>
USPT	11 and transthretin gene promoter	•	
-	11 and hnf 3 albumin promoter	2	<u>L11</u>
USPT	11 and hnf3 albumin promoter	0	<u>L10</u>
USPT		3	<u>L9</u>
USPT,PGPB,JPAB,EPAB,DWPI	13 and hnf-3 albumin promoter	-	_
USF1,FUID,SF1EDAD DWDI	13 and ttr gene promoter	3	<u>L8</u>
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USP1,FUFD,JI AD,DI AD,DI	14 and junction	15	<u>L5</u>
USPT,PGPB,JPAB,EPAB,DWP		23	<u>L4</u>
USPT PGPB, JPAB, EPAB, DWP	13 and heavy chain and light chair		<u>L3</u>
USPT,PGPB,JPAB,EPAB,DWP	12 and factor VIII	82	
USP1,PGPB,JPAB,EI AB,D W1		n 903	<u>L2</u>
USPT,PGPB,JPAB,EPAB,DWP	I 11 and pharmaceutical compositio	2336	<u>L1</u>
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OM nucleic - nucleic search, using sw model
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Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated virus vectors for expression of factor VIII by
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Best Local Similarity 100.0%; Score 934; DB 6; Length 11933;
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                                                                          11540 GTGGCAATCATGCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTC 11599
                                                                                                                                                                          11420 GTAGTAAGCGCCGCCTCTTTTCATCTCACTACCACAACGAGCGAATTAACCCATCGTTGA 11479
                                                                                                                                                                                                                                                                           11360 TOTGCCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCG 11419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
721 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                       661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
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ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                           541 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 600
                                                                                                                                                                                                                                                                                                                                                                                                                           11180 TTCCGGTATTCGCTTAATTCAGCACAACGGAAAGAGCACTGGCTAACCAGGCTCGCCGAC 11239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match

100.0%; Score 934; DB 6; Length 11933;

Best Local Similarity 100.0%; Pred. No. 1.5e-286;

Matches 934; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 gtagtaagcgccgcctcttttcatctcactaccacaacgagcgaattaacccatcgttga 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11120 TGGGTTGTGCTGCTGGGGCGGCGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC 11179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                         361 totgootgogatggttggagttocagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: US 6221349-A 13 24-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 11933)
Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated vectors for expression of factor VIII by target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unknown.
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Sequence 13 from patent US 6221349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="unknown"
2818 c 2717 g 3140 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .11933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            841 cgtcgcgcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     St Pierre,R. and Linn,T.
A refined vector system for the in vitro construction of single-copy transcriptional or translational fusions to lacz gene 169 (1), 65-68 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning vector TLF97-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning vector TLF97-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   artificial sequence; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             StPierre, R
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/db xref=""Caxon:43840"
complement(19404 .19489)
                                                                                                                                                                                                                                                                                                                               /translation="MYYLKNINEWMEGLEFEFYFEIMGAYFPEFDIWLHDINHISKSD / translation="MYYLKNINEWMEGLEFEFYFEIMGAYFPEFDIWLHDINHISKSD / TGIIFAAISLESLLEQPLEGLLSDKLGLRKYLLWIITGMLVMFAPEFIFFFGELQYN TGIIFAAISLESLLEQPLEGLSDKLGLRKYRNGAFGRARMEGCYGWALCASIVGI LVGSIVGGIYLGFERNMAAPAYEAF IEKVSRRSNFEFGRARMEGCYGWALCASIVGI MATINNQFVFWLGSGCALILAVLLFFAKTDAÞSSATVANAJGANHSAFSKLKLALELER OPKLMFLSLYVIGVSCTYDVFDQJFANFTSFEFATGBGGTRVFGYVTTMGELLNASIM OPKLMFLSLYVIGVSCTYDVFDQJFANFTSFEFATGBGTRVFGYVTLMGEVPELLVGCFFANLIVNGTGGKAKLLLAGTIMSVRIIGSSFATSALEVVILKTLHMEEVPELLVGCFFANLIVNGTGGRAYLVLGLVALGFKYLTSOFEVFSATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFEVFSATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFEVFSATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFEVFSATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFEVFSATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFEVFSATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFFTATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFFTATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFFTATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLVCFCFFRQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGFKYTTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOFFTATTYLTSOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="lactose permease"
/protein_ld="AAC53648.1"
/db_xref="GI:1066305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="lacy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="lacY"
                                                                                                                                                                                                                                                       complement(20812. .>23859)
                                                                                                                                                                                                                                                                                                         complement(20812, .23859)
                                                                                                                                                                                                                                                                                   /gene="lac2%
                                                                                                                                                               /note="EcoRI site normally present at the 3' end of lacZ has been temoved by an uncharacterized mutation"
                         /product="beta-galactosidase"
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/db_xref="GI:1066306"
                                                                                                             /transl_table=11
/translation="VVLQRRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQOLR
                                                                                                                                         /codon_start=J
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                                                                                                                                                                                                                                    38971 TGGGTTGTGCTGCTGGGCGGCGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC 38912
                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                  121 tgggttgtgctgttgctggggggggtgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                      241 tottcacgattatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                          1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
361 totgcotgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                       TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCGAAAC 38792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.8%;
Similarity 99.7%;
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AGOLMITVRVQPNATAWSEAGHISAWQOWRLAENLSVTLPAASHAIPHITSEMDFC
IELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRODGFTRAPILDNDIGVSEATRIDENAW
VERWKAAGHYQAEAALLQCTADTLADAVLTTAHAWQHQGKTLFISRKTYRIDGSGOM
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SDMYTPYVFPSENGLRCGTEELNYGPHOWRGDFOFMISRYSOQOLMETSHRHLLHAEE
GTWLNIDGFHMGIGGDDSWSPSYSAEFQLSAGRYHYQLVWCOK"
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24475. 25665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGVLLALYALMOFLCAPVLAALSDRFGRRPVLLASLLGAT DYA HATTPVLUNILLAG
YGVLLALYALMOFLCAPVLAALSDRFGRRPVLLASLLGAT BYA HATTPVLUNILLAG
RIVAGTTGATGAVAGAY IAD ITDGEDBARRHGCILMSACFGVGMVAGPVAGGLIGALSLL
RIVAGTTGATGAVAGAY IAD ITDGEDBARRHGCILMSACFGVGMVAGAMT IVAALMTV
APELAAAVLNGLUNLLGCFLMOESHKGERRPMPLRARNHVSSFRAMAGMT IVAALMTV
EFIMQLVGQVPAALMVLFGEDBRFMSATMIGLSLAVFG ILAALAQAFVFGPANKRFGE
FFIMQLVGQVPAALMVLFGEDBRFMSATMIGLSLAVFG ILAALAQAFVFGANLSROVDDDHQG
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KQAIIAGMAADALGYVLLAFATRGMMAFPIMILLASGGIGMPALQAMLSROVDDDHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="tetracycline resistance protein"
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/db_xref="GI:1066307"
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33602. .35450
substitution"
note="imm21 substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLOGSLAALTSLTSTTGPLTVTATYAASASTNNGLAWIVGAALYLVCLPALRRGAWSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10533 c 11616 g 10081 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 923.2; DB 12; Length 42529; Pred No. 4.4e-283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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REFERENCE
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                                                                                                             terminator
                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38431 TTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATATGCTGCGCTTGCTGGCATCCT 38372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38491 TTTGTGGCATTGCACCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGG 38432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 901 tgccttagtatttccttcaagctgcccc 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38551 GTGGCAATCATGCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTC 38492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38611 GTCAAATTTACCCAATTTTATTCAATAAGTCAATATCATGCCGTTAATATGTTGCCATCC 38552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38671 GTAGTAAGCGCCGCCTCTTTTCATCTCACTACCACAACGAGCGAATTAACCCATCGTTGA 38612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38731 TCTGCCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCG 38672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  601 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
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                                                                                                                                                  Submitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada
                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                             artificial sequence; vectors.

1 (bases 1 to 4253)
St Pierre, R. and Linn, T.
A refined vector system for the in vitro construction
                                                                                                                                                                                                                             StPierre, R.
                                                                                                                                                                                                                                                    single-copy transcriptional or translational fusions to lacz
                                                                                                                                                                                                                                                                                                                                                        Cloning vector TLF97-2. Cloning vector TLF97-2.
                                                                                                                                                                                                                                                                                                                                                                                                      U39285.1 GI:1066308
                                                                                                                                                                                                                                                                                                                                                                                                                                               CVU39285 42530 bp
Cloning vector TLF97-2,
                                                                                                                                                                                                                                                                                                                                                                                                                             vector, complete sequence
                                                                                                                                                                                                                                       (bases 1 to 42530)
                           /gene="lacy"
                                                    complement(19507. .20760)
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                                                                              complement(19404 . 19489)
/note="rrnBT2 terminator"
                                                                                                    /organism="Cloning vector TLF97-2"
/db_xref="taxon:43841"
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                                                                                                                                                                                                                                                                                                                                                                                                                             phage lambda lacz translational fusion
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                                                                                                BASE COUNT
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                        Query Match
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                                                                                                                         misc_feature
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1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
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/note="imm21 substitution"
                                                                                                                                                                                                                                                                                                                                                                                                     QLQG$LAALT$LT$ITGPLIVTAIYAASA$TWNGLAWIVGAALYLVCLPALRRGAW$R
                                                                                                                                                                                                                                                                                                                                                                                                                                     FFIMQLVGQVPAALWVIFGEDRFRWSATMIGLSLAVFGILHALAQAFVTGPATKRFGE
KQAIIAGMAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Translation="MKSNNALIVILGTVTLDAVGIGLVMPVLPGLLRDIVHSDSIASH
YGVLLALYALMQFICAPVLGALSDREGRRPVLLASLLGATIDYAIMATTPVLWILYAG
RIVAGITGATGAVAGAYIADITGGEDRARHFGLMSACFGVGMVAGFVAGGLLGAISLH
APFLAAAVLNGLNILLGCFLMQESHKGERRPMPLRAFNPVSSFRWARGMTIVALMTV
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/db_xref="GI:1066311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(23875. 23958)

note="multiple cloning site"
complement(23974. 24142)
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24476. .25666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK*
                                                                                   98.8%; Score 923.2; DB 12;
99.7%; Pred. No. 4.4e-283;
^. Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-galactosidase"
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/product="lactose permease"
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PTINNOFVFMLGSGCALILAVLLFFAKTDAFSSATVANAVGANHSAFSLKJALELFR
FFAPLIINNIGGKNALLAGGTMYRFTSFFATGBOGTRVFGYVTTWGELLWASIM
VTTRCORDUBERAMTVYWFRTEFFTANTEMENT AMTERMENT AMTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="lacz" .23859)
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CVU39286/c
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KEYWORDS
SOURCE
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| 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 11| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 13| | 1
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                                                                                                                CVU39286 42531 bp
Cloning vector TLF97-3,
       Cloning vector TLF97-3.
                                                     U39286.1 GI:1066312
                                                                                            vector, complete sequence
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REFERENCE
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                           CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning vector TLF97-3
artificial sequence: vectors.
1 (bases 1 to 42531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single-copy transcriptional or translational fusions to lacz gene 169 (1), 65-68 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       st pierre,R. and Linn,T. A refined vector system for the in vitro construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, gubmitted (24-OCT-1995) Thomas Linn, Microbiology and Immunology, Submitted (24-OCT-1995) Thomas Linn, Microbiology and Submitted (24-OCT-1995) Thomas Linn, Microbiology (24-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 42531)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /OD. XIELE "GLILUOGGLA"

/ translation= "VVLQRRDWENDGVTQLINRLAAHPPFASWRNSEEARTDRPSQQLR
/ translation= "VVLQRRDWENDGVTQLINRLAAHPPFASWRNSEEARTDRPSQQLR
SINGEWRFANHFPAPEAVPESWLEGCDLPEADTVVVPSNWQMHGYOAPI TIVN

SINGEWRFANHFPAPEAVERSOGSYLEDODWRRMSGIFRDVSLIHKPTQJSDFH
PPFVPTENPTGCYSLTFNUDESWLOEGGTRI I FDGVNSAFHLWCNGRWWGYGQOSTLP
SEDLISAFLRAGENRLAVMVLRWSDGSYLEDODWRRMSGIFRDVSLIHKPTQJSDFH
PFVTENDDFSRAVLEAEVQMCGELROYLRTVPSLWGGIFVQNSCGTAPFGGEI I DERGG
SEDLISAFLRAGETYNLYERVENVOLHTADGTLIEAEACDVGFREVR I ENGLL
VATRENDDFSRAVLEAEVQMCGELROYLRTVPSLWGGIFVQNSCGHPANHPSVIIWSL
LINGKPLLIRGYWRHEHHPLHGOVNDEOTMVQDILLMKQNNFNAVCSHYPNHPJMYT
YADRVTLENLNVERNEKLEDEFTANLIDEPRALPAKSERVTTRMVGDENHPSVIIWSL
LINGKPLLIRGYWRHEHHPLHGOVNDEOTMVQDILLMKQNNFNAVRDENOPEPAVP
LCDRYGLYVVDEANIETHGMVPNNRLIDDFRALPAKSERVTTRMVGDENHPSVIIWSL
LIKYDENGANHDALYRWIKSVDPSRAVVYSEGGADTTNTDII ICPMVARVDENOPEPAVP
GNESGHGANHDALYRWIKSVDPSRAVVYSEGGGADTTNTDI ICPMVARVDENOPEPARLS
KWGISLKKWLSLIPGETRPLILCEYAHAWALDGCREAEVRADFPPHPALTEALGGFVWHDWDOS
GNESGHGANHDALLHWAYALDGKPLASGEVVLDVAPOGKQLIELFPLPAPES
LIKYDENGAWSAKGGDFSGTFNDROFFCMGLYFDADFVPHPALTEALFPHAM
AGOLMITVRKVQPNATAWSEAGHTSAWQQWRLAENLSVTLPAASHATEHLTTSEMDFC
GQTILTVTSEYLFRHSDNELLHMYALDGKPLASGEVVLDVAPOGKQLIELFPLPAPE
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SDMYTPVYBPSENGLAGGTRELNYGPHQARGDFGONISKYSGONISCHONICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:43842"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="lacY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Cloning vector TLF97-3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="lacz"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="EcoRI site normally present at the 3' end of lacz has been removed by an uncharacterized mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="beta-galactosidase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl_table=11
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                                                                                                                                                                                                        /note="multiple cloning site" complement(23975. .24143)
                                                                                                                                                                                                                                                                             complement(23876
                                                                             /note="rrnBT1 terminator"
24477. .25667
/gene="tetR"
/gene="tetR"
                                                           . 25667
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38493 TTTGTGGCATTGCACCAGCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGG 38434
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721 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                                                                                     38673 GTAGTANGCGCCGCCTCTTTTCATCTCACTACCACAACGAGCGAATTAACCCATCGTTGA 38614
                                                                                                                                                                                                                                                                                                                                                                  38733 TCTGCCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCG 38674
                                                                                                                                                                                                                                                                                                                                                                                                                               38793 CGTTATGCAGGCTCTAACTATTACCTGCGAACTGTTTCGGGATTGCATTTTGCAGACCTC 38734
                                                                                                                               601 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38853 TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCGAAAC 38794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38913 TTCCGGTATTCGCTTAATTCAGCACAACGGAAAGAGCACTGGCTAACCAGGCTCGCCGAC 38854
                                                                                                                                                                                                                                                       481 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 925;
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Best Local
                                                                                                                                                                                                                                                                                                                      421 gtagtaagcgccgcctotbttcatctcactaccacaacgagcgaattaacccatcgttga 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38973 TGGGTTGTGCTGTTGCTGGGGGGGGGGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC 38914
                                                                                                                                                                                                                                                                                                                                                                                   361 totgootgogatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 tottoacgattatogactcaatgotottacotgttgtgcagatataaaaaatcocgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 aaaggecgeagegtaactattactaatgaatteaggaeagaeagtggetaeggeteagtt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="tetracycline resistance protein"
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KOALIAGWAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
ROALIAGWAADALGYVLLAFATRGWMAFPIMILLASGGIGMPALQAMLSRQVDDDHQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="imm21 substitution" 10534 c 11615 g 10082 t
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.8%; Score 923.2; DB 12; Length 42531; 99.7%; Pred. No. 4.4e-283;

 Mismatches

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REFERENCE
AUTHORS
TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38253 CGTCGCGGCACTACGGCAATAATCCGCATAAGCGAATGTTGCGAGCACTTGCAGTACCTT 38194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38313 TGTTTTGGCAATATCAACCGCACGGCCTGTACCATGGCAATCTCTGCATCTTGCCCCCGG 38254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38373 TGAATAGCCGACGCCTTTGCATCTTCCGCACTCTTTCTCGACAACTCTCCCCCCACAGCTC 38314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       901 tgccttagtatttccttcaagctgcccc 928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 tyttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgccccgg 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-SBP-1995) Thomas Linn, Microbiology and Immunology, University of Western Ontario, London, Ontario N6A5C1, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 42704)
StPierre,R. and Linn,T.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial sequence; vectors.

1 (bases 1 to 42704)

St Pierre, R. and Linn, T.

A refined vector system for the in vitro construction of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single-copy transcriptional or translational fusions to lacz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning vector lambda TXF97. Cloning vector lambda TXF97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVU37692 42704 bp DNA SYN 13-APR-1996 Cloning vector lambda TXF97, lac2 transcriptional fusion vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U37692.1 GI:1051181
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/note="EcoRI site normally present at the end of lac2 has been removed by an uncharacterized mutation"
                                                                 complement(20812. .23886)
/gene="lacz"
                                                                                                              complement(20812.
/gene="lacz"
                                                                                                                    TLISVFTLSGPGPLSLLRRQVNEVA "complement(20812. .23886)
                                                                                                                                     KYITSQFEVRFSATIYLVCFCFFKQLAMIFMSVLAGNMYESIGFQGAYLVLGLVALGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                            removed by an uncharacterized mutation*
complement(19404, 19489)
/note="rrnBf2 terminator"
                                                                                                                                                                                                                                                                                                                                                                                                           complement(19507. .20760)
                                                                                                                                                                                                                                                                                                                                                                                                    /gene="lacy"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="lacy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="BamHI site normally present at this site has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           removed by an uncharacterized mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="EcoRI site normally present at this site has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Cloning vector lambda TXF97"
/db_xref="taxon:43300"
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BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 925; Conservative
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/product="beta-galactosidase"
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Bacteriophage lambda, complete gen
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                                                                                                                                                                                                                                                                                                                               DNA-binding protein; circular; coat protein; complete genome; origin of replication; repressor; unidentified reading frame.
                                                                                                  Lebowitz, P., Weissman, S.M. and Radding, C.M.
Nucleotide sequence of a ribonucleic acid transcribed in vitro from lambda phage deoxyribonucleic acid transcribed in vitro from lambda phage deoxyribonucleic acid lambda phage acid lambda phage deoxyribonucleic acid lambda phage acid 
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                                                  Deletions of lambda phage locating a prm mutation within the
                                                       rightward operator
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                                                                                          12 (bases 37946 to 38039)
Smith, G.R., Eisen, H., Rei
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                                                                                                                                                                                                                  Walz,
                                                                                                                                          Lambda repressor regulates the switch between PR and Prm promoters
                                                                                                                                                                                                                                                                                                                                                                                         Maniatis,T., Jeffrey,A. and Kleid,D.G.
Nucleotide sequence of the rightward operator of phage lambda
Proceedings of the National Academy of Sciences of the United
States of America. 72 (3), 1184-1188 (1975)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dahlberg, J.E. and Blattner, F.R. Sequence of the promoter-operator proximal region of the major leftward RNA of bacteriophage lambda Nucleic acids research. 2 (9), 1441-1458 (1975)
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Kleid,D.G., Agarwal,K.L. and Khorana,H.G.
The nucleotide sequence in the promoter region of the gene N in bacteriophage lambda
                                                                                                                                                                                          (bases 37905 to 37989) lz.,A., Pirrotta,V. and Ineichen,K.
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Maniatis,T., Ptashne,M., Backman,K., Kield,D., Flashman,S.,
Jeffrey,A. and Maurer,R.
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VIRUS RESEARCH. PROCEEDINGS OF 1973 ICN-UCLA SYMPOSIUM: 533-544;
Cademic Press, New York (1973)
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In vitro transcription products of lambda DNA: Nucleotide sequences
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Nature New Biol. 233, 230-231 (1971)
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24 (bases 37938 to 38016; 35589 to 35666)
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                                                                178-Nucleotide sequence surrounding the cos site of bacteriophage
                                                                                                  23 (bases 13 to 72; 48391 to 48502) Nichols, B.P. and Donelson, J.E.
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Control of transcription termination
Annual review of biochemistry. 47, 967-996 (1978)
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78054731
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Denniston-Thompson,K., Moore,D.D., Kruger,K.E., Furth,M.E. and
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Davies, R.W., Schreier, P.H. and Buchel, D.E.
Nucleotide sequence of the attachment site of coliphage lambda
Nature, 270 (5639), 757-760 (1977)
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Roberts,T.M., Shimatake,H., Brady,C. and Rose
Sequence of Cro gene of bacteriophage Lambda
Nature. 270 (5634), 274-275 (1977)
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DNA base sequence of the po promoter region of phage lamdba
Paranana 265 (5590), 117-121 (1977)
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Ptashne,M., Backman,K., Humayun,M.Z., Jeffrey,A., Maurer,R.,
Meyer,B. and Sauer,R.T.
Autoregulation and function of a repressor in bacteriophage lambda
Science. 194 (4261), 156-161 (1976)
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Nucleotide sequence of cro, cII and
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Determination of the endpoints of partial deletion mutants of the
attachment site of bacteriophage lambda by DNA sequencing
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Cloning vector lambda
U02453
                                                                                       Submitted (07-CCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA 1020 East Meadow Circle, Palo Alto, CA 94303, USA This sequence has been compiled from information in the sequence databases, published literature and other sources. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECHECLONTECH.COM.
                                                                                                                                                                                                                                                                                          Frischauf,A.M., Lehrach,H., Poustka,A. and Murray,N. Lambda replacement vectors carrying polylinker sequences J. Mol. Biol. 170 (4), 827-842 (1983)
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                                                                           Location/Qualifiers
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Matches 924;

Conservative

0;

Mismatches

98.7%;

Score 921.6; DB 12 Pred. No. 1.4e-282;

DB 12;

Length 9170;

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Gaps

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Local Similarity

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                                                     Cloning vector lambda
Cloning vector lambda
                               U02427.1
                                                                        XXU02427
                               GI:413793
                                                                       9205 bp
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 EMBL3 SP6/T7
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661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
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                                                                                                                           gfggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc
                                    TTTGTGGCATTGCACCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGG 5108
                                                                                                         GTGGCAATCATGCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTC
                                                          tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                                                                                            GTCAAATTTACCCCAATTTTATTCAATAAGTCAATATCATGCCGTTAATATGTTGCCATCC
                                                                                                                                                                                             gtcaaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-0CT 1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Cirlce, Palo Alto, CA 94303, USA
This sequence has been compiled from information in the sequence databases, published literature and other sources. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECHGCLONTECH.COM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning vector lambda EMBL3 SP6/T7 artificial sequence; vectors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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                                                                                                                                                             616
                                                                                                                                                                        186 gtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgactcttc 245
                                                                                                                                                                                                                                                                            66 ccgcagcgtaactattactaatgaattcaggacagacagtggctacggctcagtttgggt 125
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                                                                                                                     246 acgattatcgactcaatgctcttacctgttgtgcagatataaaaaaatcccgaaaccgtta 305
306 tgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctctctgc 365
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bacteriophage lambda
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1 (bases 1 to 735)
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/db_xref="taxon:10710"
                                                                                                                                                                                                                                                                                                                                     70.4%; Score 657.4; DB 7; Length 735; 98.2%; pred. No. 2.9e-198;
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 Mismatches

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                  516 tcatgccgttaatatgttgccatccgtggcaatcatgctgctaacgtgtgaccgcattca 575
                                                             Match 48.0%; Score 448.2; DB 7; Length 751; Local Similarity 98.1%; Pred. No. 1.7e-131;
                                                                                                                                                                                                                                                                                                                                                                     LAMQPR 751 bp DNA PHG Bacteriophage lambda Q protein gene, complete cds
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bacteriophage lambda
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1 (bases 1 to 751)
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                                                         Conservative
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                                                                                                                                /organism="bacteriophage lambda"
/db_xref="taxon:10710"
                                                                                                                YRAVTMLIPNLTOPTWSRTYKPLYDALVVQCHKEESIADNILNAITR"
1 168 c 209 g 162 t
                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                               Atkinson, B.L. and Gottesman, M.E.
The Escherichia coli rpo860 mutation blocks antitermination by coliphage HK022 Q-function
J. Mol. Biol. 227 (1), 29-37 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (05-SEP-1991) B.L. Atkinson, Columbia Univ College of Physicians and Surgeons, 701 West 168th. Street, New York NY 10032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterobacteria phage HKO22.
Enterobacteria phage HKO32
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
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antitermination block: Q gene; rpoB60; rpoB60 mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Atkinson, B.L
                                                                                                                    /db_xref="Sptrembl:002582"
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                                                                                                                                                                                                                                                                           /gene="Q":
34 . .657
/gene="Q":
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/db_xref="taxon:10742"
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                                                                             Submitted (31-MAY-1998) Pittsburgh Bacteriophage Institute & Dept. of Biological Sciences, University of Pittsburgh, Pittsburgh, PA
                                                                                                                                                                                                           Genomic sequences of bacteriophages HK97 and HK022: pervasive genetic mosaicism in the lambdoid bacteriophages
J. Mol. Biol. 299 (1), 27-51 (2000)
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                                                                                                                                          2 (bases 1 to 40751)
Juhala,R., Ford,M.E., Duda,R.L., Youlton,A., Hatfull,G.F. and
                                                                                                                                                                                                        10860721
                                                                                                                                                                                                                                                                    Lambda phage group.

(bases 1 to 40751)

Juhala,R.J., Ford,M.E., Duda,R.L., Youlton,A., Hatfull,G.F. and
                                                                                                                                                                                                                                                                                                                   Enterobacteria phage HK022.
Enterobacteria phage HK022
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
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Bacteriophage HK022, complete genome.
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/db_xref="taxon:10742"
                      /organism="Enterobacteria phage нк022"
                                                                 Location/Qualifiers
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95.18;
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/note="gp
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/transl_table=11
/evidence=not_experimental
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/protein_id="Aterminase large subunit"
/protein_id="Aterminase large subunit"
/protein_id="Aterminase large subunit"
/db_xref="G1:6863113"
/d
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/protein_id="AAF30353:1"
/db_xref="GI:6863112"
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NIRSKALDSWTPADLLAAVELANNQLYITVLRKDLRKEERIRGEERDEGLIKDLRKQI
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5219...5545
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KEYWORDS
                                                                                          VERSION
                                                                                                          ACCESSION
                                                                                                                           DEFINITION
                                                                                                                                                       AF335538/c
                                          ORGANISM
                                                                                                                                                                                                    36574 GGCAATCTCTGCATCTTGCGCCCGGTGTCGCGGCACTACGGCAATAATCCGCATAAGCGA 36515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 450;
                                                                                                                                                                                                                                                                                                                                                                                                   36874 TCATGCCGTTAATATGTTGCCATCCGTGGCAATCATGCTGCTAACGTGCGCACCGCATTCA 36815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36934 AACGAGTGCATTTATCCATCGTTGGGTCAAATTTACCCAACTTTATTCAAAAAGTCAATA 36875
                                                                                                                                                                                                                                                                                                                                                      756 totogacaactotocococacagototgttttggcaatatoaacogcacggcotgtaccat 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 aacgagcgaattaaccca#cgttgagtcaaatttaccccaattttattcaataagtcaata 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 tcatgccgttaatatgttgccatccgtggcaatcatgctgctaacgtgtgaccgcattca 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                     Viruses; dsĎNA viruses, no RNA Stage; Tailed phages; Siphoviridae.
                                                                             AF335538.1 GI:13517559 .
                                     Bacteriophage
                                                 Bacteriophage HK620
                                                                                                          Bacteriophage HK620, complete genome.
                                                                                                                                      AF335538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                 38297 bp .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product="lambda gpT analog"
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RERYCSLNPMLRVEWGAGLVSSMIANVNRDFKRPPFNPTDFTLHFTKVKAADGPISLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="gp14; presumed to be expressed as the downstream part of a translational frameshift product; start is placed at the presumed frameshift site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8478. .10898
/note="gp16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Product="lambda gpg analog"
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/product="lambda gpg analog"
/product="naps30365.1"
/db_xref="gf1:6863124"
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LAIQEVNDLGKTSSAPKTNSGASSSSTESEAEQSPKRGKSSHSKSPNSGQSTGNDTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
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                                   HK620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.7%; Score 436.2; DB 7; Length 40751; 95.1%; Pred. No. 1.2e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                 DNA
                                                                                                                           circular PHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clark, A.J., Inwood, W.B., Cloutier, T. and Dhillon, T.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clark, A.J., Inwood, W.B., Cloutier, T. and Dhillon, T.S.
Nucleotide Sequence of Coliphage HK820 and the Evolution of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lambdoid Phages
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                                       complement(1664 . .1702)
/function="phage integration"
complement(1689 . .1701)
                                                                                                                                           RARWLYRDHCEFKNKLLSRANG"
/bound_moiety="cII protein"
                                                                                                                                                       /translation="MQHELQPDSLVDLKFIMADTGFGKTFIYDRIKSGDLPKAKVIHG
                                                                                                                                                                                                                              /protein_id="AAK28851.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1457. .1657)
/gene="hkaC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="hkaC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1368.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="attP core"
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/gene="hkaB"
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/gene="hkaB"
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/product=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAK28850.1"
/db_xref="GI:13517561"
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/transl_table=11
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LLTTLSSITKPVSEFVFAGRNDKKKPICENAVLLVIKQIGYEGLESGHGFRHEFSTIM
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complement(join(1. .23,38289. .38297))
/note="terminator for prophage excision transcript; xIS"
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/gene="int"
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/gene="hkaD"
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/gene="hkaf"
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/gene="hkaE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to eaG of Bacterophage P22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="hkaD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /function="promoter activation to establish lysogeny"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GASWKPSHWMPLPEPPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2601. .2792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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NEEIALTYGRLRVELEGKDSKIANLTAERDALREGEWGDARHSNTRAAADIYFQLVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(2794. .3510)
/gene="hkaG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="hkaF"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterfophage P22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="hkaG"
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                                                                                                                                                                                                                                                                                         YKVSEVIAAIRAAGIRIKGE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEIPAGGSLVEYVDDMREKLEAAEKRIAELEDREILLPERSSMLHRTDFHDDYQTVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3507. .3989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene=∦hkaH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(3507. .3989)
                                                                                                                                                                                              complement(3986. .4150)
                                                                                                                                                                                                                                                             DAFLAEVRAQGVEMYADNLDNVADDAERGGFDYAVKFLRSEASSVRLFADQLRKGGSQ
                                                                                                                                complement(3986. .4150)
                                                                                                                                                            /gene="hkaI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="hkaH"
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                           /transl_table=11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  516 tcatgccgttaatatgttgccatccgtggcaatcatgctgctaacgtgtgaccgcattca 575
                                                                                                                                                                636 gcttaacagtgcgtgaccaggtgggttgggtaaggtttggggattagcatcgtcacagcgc 695
756 totogacaactctcccccacagctctgttttggcaatatcaaccgcacggcctgtaccat 815
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                                                                                                                                             GCTTAACAGTGCGTGACCAGGTGGGTTGAGTAAGGTTTGGGATTAGCATCGTTACAGCGC 15378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4045.
/note="tL3"
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/gene="hkaJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4481. .5068)
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/product="unknown"
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/gene="hkaL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANMVASLKDKDNRSKNVSQNHADDYGYSQNDYPPF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(5754. .5942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HQIKENAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTIVLRTLTRDDQFFFTTKNNGADTVKSPMGMFDSNEIDNDLSFVDATVCDYYGINNV
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94.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 429.8; DB 7; pred. No. 1.4e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4457)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 38297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAATCTCTGCATCTTGCGCCCGGGGGTCGCGGCACTACGGCAATAATCCGCATAAGCGA 15198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99caalctctgcatcttgcccccggcgtcgcggcactacggcaataatccgcataagcga 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUN-1998) Pittsburgh Bacteriophage Institute & Dept. of Biological Sciences, University of Pittsburgh, Pittsburgh, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hendrix, R.W..
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Juhala, R., Ford, M.E., Duda, R.L., Youlton, A., Hatfull, G.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic mosaicism in the lambdoid be J. Mol. Biol. 299 (1), 27-51 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequences of bacteriophages HK97 and HK022: pervasive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage HK97, complete genome. AF069529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Juhala,R.J., Ford,M.E., Duda,R.L., Youlton,A., Hatfull,G.F. and Hendrix,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Lambda phage group.
1 (bases 1 to 39732)
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Bacteriophage нК97
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542. .205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence-not_experimental / product="terminase small subunit" / protein_id="Ass1097.1" / protein_id="Ass1097.1" / protein_id="Ass1097.1" / db_xref="G1:6901594" / translation="MADKRIRSDSSAAAVQAMKNAAVDTIDPPSHAGLEKKAEPFWHD / translation="MADKRIRSDS"" / translation="MADKRIRSDS" / transla
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50. .53
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3348. .402
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LNPRDWHNIALLKDNEGRYIFGGPQAFTSNIMWGLPVVPTKAQAAGTFTVGGFDMASQ
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2056. .3330
/gene="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLPGGDVAMRQAQYVPITDLGTNKEPRNNGA"
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DQFRKDADAIGLSLPLVEFGQGFKDMGPAVDTLESLMLNGRVRHGMHPVLTMCAVNAV
VVKDAAGNRKLDKSKATGRIDGNVAMTMSVGAANGEVTEQGGDEDDFIFRPLSM*
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5545.
        Conservative
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/gene="10"
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                                                                                                                                                                            note="putative".
                          45.7%;
95.1%;
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 Mismatches

                                Pred. No.
                                                Score 426.8;
                5.8; DB 7;
. 1.2e-124;
tches 22;
                                                    Length 39732;
                    Indels
                    1; Gaps
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                                                                       35560 TGGCAATCTCTGCATCTTGCGCCCGGCGTCGCGGCACTACGGCAATAATCCGCATAAGCG
                 815 tggcaatototgcatottgcccccggcgtcgcggcactacggcaataatccgcataagcg 874
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Search completed: January 8, 2002, 17:22:58 Job time: 12469 sec

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OM nucleic - nucleic search, using sw model '.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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934
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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES .

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934 934 36.6 33 32 31.8 31.8 31.8 31.8	score
100.0 100.0 3.9 3.5 3.4 3.4 3.4 3.4 3.4	Query Match
11933 11933 37856 1063 49617 469 469 469 542 542	Query Match Length DB
222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222 222	B 1D
AAD00121 AAD08612 AAA11992 AAC37411 AAF28541 AAI12818 AAI34173 AAI02735 AAI02735 AAI18836 AAI43958 AAF58252	ID
Human factor VIII S. cellulosum DNA Arabidopsis thalia Genomic fragment # Probe #2751 for ge Probe #2756 used t Probe #2766 used t Probe #3769 for ge Probe #3769 for ge Probe #12644 used Oligonucleotide D1	Description Recombinant adeno

Couto LB, Colosi PC; (AVIG-) AVIGEN INC.

WPI; 2000-339536/29.

New recombinant adenovirus-associated vector, useful for gene therapy

30.4.008	37 30.8 38 30.8 39 30.8	30.8 30.8	31 31.2	27 31.4 28 31.2 29 31.2	31.4 31.4 31.4 31.4 31.4 31.4	31.8 31.8 31.8 31.6 66.8 88.8 88.8	12 31.8 13 31.8 14 31.8 15 31.8
3 34990 3 387 3 1073 3 113 69 2 118	3 1951 3 1952 3 6528	3 1951 3 1951 3 1951	4870 3 642 3 822	2940 18 3691 18 4147 18	936 22 936 22 936 22 938 22	1698 19 4455 18 8709 22 8707 21 4668 19	936 22 . 936 22 . 936 22 .
AAQ115 AAA105 AAA390 AAC750 AAC980	AAZ91005 AAZ49723 AAH68527	AAC9444 AAT4950 AAV2144		AAT90501 AAT90500 AAT68934	AAF58254 AAF58257 AAF58259 AAF58262 AAF58255	AAX30577 AAV25095 AAF25628 AAC26010 AAV60918 AAF58252	AAF58254 AAF58257 AAF58259 AAF58262 AAF58255
Gene encoding a su Human secreted pro Human ORFX ORF1237 Human colon cancer	H. influenzae stra Staphylococcus sim C glutamicum codin	in recep	C glutamicum codin Corynebacterium gl Bacterial transfer	Signalling inosito GRB2 associating p Human SH2-containi	Oligonucleotide D1 Oligonucleotide D2 Oligonucleotide D2 Oligonucleotide D1 Oligonucleotide D1 Signalling inosito	H. pylori secreted H. pylori HPN165 H. pylori HPN165 H. pylori HPN165 Human secreted pro Anglogenin gene. Oligonuclectide D1	

ALIGNMENTS

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AADOO121
AAD00121 standard; DNA; 11933 BP.
                                                                                                                      Recombinant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor VIII; heviII; HNF-3 albumin promoter; human elongation factor lalpha; Erlalpha; human growth hormone; hGH; inverted terminal repeat; ITR; haemophilia; gene therapy; ds.
                                                                                                                                                                                                                     AAD00121;
                                                                                                                                                                           Recombinant adeno associated vector construct, PAAV-F8-1.
                                                                                                                                                                                                31-JUL-2000 (first entry)
         20-OCT-1998;
24-MAR-1999;
                                                                                 WO200023116-A1.
                                                                                                     Adeno associated virus.
                                                             27-APR-2000.
  30-JUL-1999;
                                         19-OCT-1999;
    98US-0104994.
99US-0125974.
99US-0364862.
                                              99WO-US24495
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11540 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 11599
                                                                                                                                                                                                        11480 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 11539
                                                                                                                                                                                                                                                                                     11360 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 11419
                                                           541 gtggcaatcatgctgctaacgfgtgaccgcattcaaaatgttgtctgcgattgactcttc 600
                                                                                                                                                                                                                                                                                                                                                                            11300 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcatttttgcagacctc 11359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 934;
601 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11240 tetteaegattategaeteaatgetettaeetgttgtgeagatataaaaaateeegaaae 11299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                          481 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11180 ttccggtattcgcttaattcmgcacaacggaaagagcactggctaaccaggctcgccgac 11239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11120 tgggttgtgctgttgctggggggggatgacgcctgtacgcatttggtgatccggttctgc 11179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 totgootgogatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11000 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 11059
                                                                                                                                                                                                                                                                                                                                                                                                301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 tottoacgattatcgactcaatgotottacotgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hFVIII coding region comprises the heavy chain gene segment with the and 5 amino acids from the N-terminus of the B domain. The light chain into the segment is segment with the heavy and 1 segment with the segment comprises the C-terminal 85 amino acids of B domain are cloned to the B domain. Both the heavy and light chain segments are cloned control segmences, that directs the transcription and translation of the B domain, that is deletted. This plasmid is operably linked to therapeutic levels of Factor VIII gene. The adeno-associated viral vectors are used for gene therapeutic levels of Factor VIII in vivo. The rAAV are used for gene therapy, because of their broad host range, safety profile and duration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 tgggttgttgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present DNA sequence is a recombinant adenovirus associated vector, than the first intron (-573 to +985) of human elongation factor lalpha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII) is inserted between the AAV inverted terminal repeat (ITR) regions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Fig 5; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 934; DB 21; 100.0%; Pred. No. 4.9e-312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 11933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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δÃ B δδ В ρy В

В δÃ Вþ Ş В Qy В Qy 밁 δÃ B Ωy В

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AAD08612
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administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a sequence encoding the heavy chain of factor VIII and a sequence encoding the heavy chain of factor VIII. The rAAV vector is expression of biologically active clotting factor VIII in mammals, in expression of biologically active clotting factor VIII in vivo. The present sequence is paav-F8-1 vector without the plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                  The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises
                                                                                                                                                                       Claim 18; Fig 5; 90pp; English.
                                                                                                                                                                                                   Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood
                                                                                                                                                                                                                                                                    WPI; 2001-417955/44.
                                                                                                                                                                                                                                                                                                   Couto LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric - Adeno associated virus.
Chimeric - Mus sp.
Chimeric - Homo sapiens.
Chimeric - Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                          (AVIG-) AVIGEN INC.
                                                                                                                                                                                                                                                                                                                                                          22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                              21-DEC-2000; 2000WO-US34925
                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200145510-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11900 tgccttagtatttccttcaagctgcccctgcagg 11933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11840 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 11899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII; blood clotting disorder; gene therapy; haemophilia A; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11780 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 11839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD08612 standard; DNA; 11933 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11720 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 11779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11660 ttgggtaaggittgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 11719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             901 tgccttagtatttccttcaagctgcccctgcagg 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgccccgg 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      721 tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 ttgggLaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         backbone. It comprises HNF-3 mouse albumin promoter, a synthetic intron based on human elongation factor lalpha (EFlalpha) and immunoglobulin G based on human factor VIII coding (IIGG) intron sequences, p-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV sequence poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both the light and heavy chains of human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11240 tetteaegattategaeteaatgetettaeetgttgtgeagatataaaaaateeegaaac 11299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11180 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 11239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11933 BP; 3258 Å; 2818 C; 2717 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11360 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 11419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11420 gtagtaagegeegeetetttteateteactaceacaaegagegaattaaeceategttga 11479
                                                                                                                                                                                                                                                                                                                                                                                                                                    11480 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 11539
                                                                                                                                                                                                                                                                                       11600 trtgrggcattgcaccaccagagtgtcatacagcggcttaacagtgcgtgaccaggtggg 11659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 aaaggeegeagegtaactattaetaatgaatteaggacagaeagtggetaeggeteagtt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                   11780 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg
                                                                                                                                            11720 tgaatagoogacgcotttgcatottccgcactotttctcgacaactctcccccacagctc 11779
                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 gtagtaagcgccgcctcttttcatctcactaccacaacgagcgaattaacccatcgttga 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
                                                                                                                                                                                                                                                                                                                                                                                   541 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 600
                                                                                                                                                                                                                                    661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
             841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tetteaegattategaeteaatgetettaeetgttgtgeagatataaaaaateeegaaae 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 11359
                                                                                                                                                                                                                                                                                                                                                                 gtggcaatcatgctgctaaggtgtgaccgcattcaaaatgttgtctgcgattgactcttc 11599
                                                                                                                                                                                                                                                                                                           tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                                                                            tgaatagccgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                  ttgggtaaggtttgggattaqcatcgtcacagcgcgatatgctgcgcttgctggcatcct 11719
                                                                                       tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 840
cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 11899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 11933;
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XXTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S. cellulosum DNA encoding polyketide and hereropolyketide enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plant-protection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epothilone; cytotoxic; immunosuppressant; antibiotic; antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polyketide biosynthesis; heteropolyketide biosynthesis; mutasynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3398..6100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8433..9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (6374..7111)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/product= "ORF1-tRNA synthetase"
/note= "gtg Start codon"
/note= "gtg Start 71111
                                                                                                                                                                                                                                                                       /_____g g /ore7-peptide synthetase"
/product= "ORE7-peptide synthetase"
28251..29400
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                          9855..11393
                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ORP4- tyrosine/DOPA-Decarboxylase"
/note= "GTG start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "ORF2-monooxygenase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                      /product= "ORF6-polyketide synthase"
20003..27889
                                                                                                                                                                                                                                                                                                                                                                                /product= "ORF5-3-oxoacyl-ACP-reductase'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "AGT start codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "ORF3-aminotransferase"
                                                                                                                                                                                                                                                    /product= "ORF8-transpeptidase" complement (30040..31720)
                                                                                                                                                                                                                                                                                                                                                             15374..19984
                                                                                                                                                                                                                                                                                                                                                                    /note= "ACC start codon"
                                                                                                                                                                /product= "ORF10-transcription regulator" 33128..33613
                                                                                                                                                                                                                           /product= "ORF9-regulation element"
                                              /product= "ORF13-transcription regulator" complement (35730..36242)
                                                                                 complement (35255..35616)
                                                                                                                                 /product= "ORF11-regulation element"
/note= "GTG start codon"
                                                                                             /product= "ORF12-regulation element"
            /product= "ORF14-transcription regulator"
/note= "GTG start codon"
                                                                                                                                                                                                                    "CGC stop codon"
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DE19846493-A1.

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RESULT
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05-MAR-1999;
09-MAR-1999;
                                                              25-FEB-2000; 2000EP-0301439
                                                                                                                                                                                                                                                                                       25127 gggcatctcgcgctggagctcgagcagccgcggccctacggcgatta 25173
                                                                                      06-SEP-2000.
                                                                                                         EP1033405-A2
                                                                                                                                    Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                             25067 tcgacacaaatcttgctcaaagaagtgttcacgctctacgaggcgcaccgcgggacaccgt 25126
                                                                                                                           Arabidopsis thaliana
                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 17282.
                                                                                                                                                                                                      17-OCT-2000 (first entry)
                                                                                                                                                                                                                                AAC37411;
                                                                                                                                                                                                                                             AAC37411 standard; DNA; 1063 BP.
                                                                                                                                                                                                                                                                                                   816 ggcaatctctgcatcttgcccccggcgtcgcggcactacggcaataa 862
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37856 BP; 5655 A; 13666 C; 12913 G; 5622 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or immunosuppressant and antiblotic and antifungal activities and are useful as plant-protection agents. This sequence represents the DNA sequence isolated from Sorangium cellulosum which is described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            products effect or are involved in the enzymatic biosynthesis, compounds (II). (I) can be inserted into an expression vector and used to transform or transfect prokaryotic or eukaryotic cells with the aim of obtaining strains that produce large amounts of polyketide or heteropolyketide compounds, especially epothilones, which have cytotoxic
                                                                                                                                                                                                                                                                                                                                               756 tetegacaactetecceeacagetetgttttggcaatateaacegcaeggeetgtaecat 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                 method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel DNA sequence (I) whose expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 20-33; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA sequence coding for products involved in the biosynthesis of polyketide or heteropolyketide compounds, especially epothilone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beyer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GBFB ) GES BIOTECHNOLOGISCHE FORSCHUNG MBH:
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                                                                                                                                                                                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mueller R;
            99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                      3.9%;
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28-JUN-1999;
29-JUN-1999;
30-JUN-1999;
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23-JUN-1999;
23-JUN-1999;
                           12-JUL-1999;
13-JUL-1999;
                                                08-JUL-1999;
09-JUL-1999;
                                                                   06-JUL-1999;
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14-MAY-1999
14-MAY-1999
14-MAY-1999
14-MAY-1999
18-MAY-1999
19-MAY-1999
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07-MAY-1999
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21-APR-1999;
                                99US-0142803.
99US-0142920.
99US-0142977.
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99US-0140991
99US-0141287
99US-0141287
99US-0141842
               99US-0143542
99US-0143624
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99US-0139750.
99US-0139763.
99US-0139817.
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990S-0139461
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99US-0140354.
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99US-0137502.
99US-0137724.
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99US-0134219

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99US-0132485
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99US-0126785
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19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999;

99US-0144086. 99US-0144325. 99US-0144331. 99US-0144333. 99US-0144333. 99US-0144334. 99US-0144352. 99US-0144352. 99US-0144632. 99US-0144632. 99US-0146884. 99US-0145086. 99US-0145086. 99US-0145088. 99US-0145088. 99US-0145088. 99US-0145087.

16-JUL-1999; 19-JUL-1999; 19-JUL-1999;

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Best Local S
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12-OCT-1999;
13-OCT-1999;
13-OCT-1999;
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14-OCT-1999;
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21-OCT-1999;
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21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
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21-OCT-1999;
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                                                                                                                                                                        AAF28541 standard; DNA; 49617 BP
                                                                                                                                                                                                                                           466 ttaacccatcgttgagtcaaatttacccaattttattcaataagtcaatatcatgccgtt 525
                                                                                                                                         04-APR-2001 (first entry)
                                                                                                                                                         AAF28541;
                                                                                                                                                                                                             986 tgcctttatgtcttcat 1002
                                                                                                 Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
                                                                                                                        Genomic fragment #28.
                                                                                                                                                                                                                       586 tgcgattgactcttctt 602
                                                                                   Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                      WO200078968-A2
      (INCY-) INCYTE GENOMICS INC
                     18-JUN-1999; 99US-0140121
                                      16-JUN-2000; 2000WO-US16649
                                                     28-DEC-2000.
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990S-0158263
990S-0159293
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990S-0159329
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990S-0159338
990S-0159638
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99US-0160767.
99US-0160768.
99US-0160770.
99US-0160814.
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99US-0160981.
99US-0161404.
99US-0161404.
99US-0161405.
99US-0161359.
99US-0161360.
99US-0161361.
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99US-0161992.
99US-0161993.
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                                                                                                                                                                                                                                                                                                                                             99US-0162142
                                                                                                                                                                                                                                                                                                                      3.5%;
                                                                                                                                                                                                                                                                                                              Score 33; DB 21; Length 1063; pred. No. 0.88; 0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                        Gaps
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10-AUG-1999; 11-AUG-1999; 12-AUG-1999; 13-AUG-1999; 13-AUG-1999;

99US-0148319 99US-0148341 99US-0148565 99US-0149368 99US-0149375 99US-0149722 99US-0149723 99US-0149723 99US-0149723 99US-0149929 99US-0149929 99US-0149929 99US-0149930 99US-0150566 99US-015066

16-AUG-1999;
18-AUG-1999;
18-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
25-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
30-AUG-1999;
31-AUG-1999;
31-SEP-1999;
31-SE

990S-0154080
990S-0151080
990S-0151308
990S-0151308
990S-0151307
990S-0153070
990S-0153070
990S-0154018
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990S-015486
990S-0156486
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990S-0156596
990S-0156486
990S-01565896
990S-01575373
990S-0156588

99US-0158029:

20-JUL-1999;
20-JUL-1999;
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21-JUL-1999;
22-JUL-1999;
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28-JUL-1999;
28-JUL-1999;
29-AUG-1999;
04-AUG-1999;
05-AUG-1999;
06-AUG-1999;
06-AUG-1999;
06-AUG-1999;
07-AUG-1999;
08-AUG-1999;
09-AUG-1999;
09-AUG-1999;

99US-0145192. 99US-0145145.

99US-0145218.

99US-014524 99US-0145276 99US-0145918 99US-0145919 99US-0145951 99US-0146386 99US-0146388 99US-0147204 99US-0147204 99US-0147204 99US-0147302 99US-0147303 99US-0147303 99US-0147260 99US-0147260 99US-0147260 99US-0147260 99US-0147260 99US-0147260 99US-0147260 99US-0147260

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RESULT 6
AAI12818/c
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                                                                                         04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
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                                                                                30-JUN-2000;
                                                                                                                            30-JAN-2001; 2001WO-US00670.
                                                                                                                                                                                                                                                                                                                                                                                                                 11682 cggatgag 11689
                                                         21-SEP-2000;
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                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                  WO200157278-A2
                                                                                                                                                                                                                               Probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                      Probe #2751 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                11622 tgggtcgtatgacagtgactttaggcgctacttctgcaccacaagcggctgatacaacaa 11681
                                                                                                                                                                                                                                                                                              12-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                AAI12818 standard; DNA; 469 BP
                                                                                                                                                                                                                                                                                                                               AAI12818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention the triplets to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see specification e.g. is useful.for aidentifying diagnostic and therapeutic compositions. M. catarrhalis. (Branhamella catarrhalis) is a large aerobic, gram-negative diplococcus, normally found among the bacterial localised infections such as ottis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                          637 cttaacag 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                              577 aatgitgictgogattgactcttctttgiggcattgcaccaccagagogicatacagogg 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 catgoogttaatatgttgooqtoogtggggaatcatgotggtaacgtgtgaccgcattcaa 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 49617 BP; 14572 A; 9853 C; 11026 G; 14166 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 235-247; 545pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-041427/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68;
                                       2000US-0608408
2000US-0632366
2000US-0234687
2000US-0236359
                         2000GB-0024263.
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
                                                        WPI; 2001-488897/53.
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                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                     Penn SG, Hanzel DK,
                                                                                                                                                  04-OCT-2000;
                                                                                                                                                            30-JUN-2000; 2000US-0508408:
03-AUG-2000; 2000US-0632366:
21-SEP-2000; 2000US-0234687:
27-SEP-2000; 2000US-0236359:
                                                                                                                                                                                            30-JUN-2000;
03-AUG-2000;
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26-MAY-2000; 2000US-0207456.
                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                 09-AUG-2001
                                                                                                                                                                                                                                                                                                                              WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                   Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                            Probe #2859 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 cgcatttggtgatccggttotgcttccggta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 CAGACAGAAGCAGAGTTGAGTGGGGGGGGGTGCTGGTTGCTTGGAGGACAAGTGGCAAGTC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID No 2751; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 cagacagtygctacggctcagtttyggttytgctgttyctgggcggcgatgacgcctgta 157
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Local Similarity 59.3%; Pr
Conservative 0;
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                                                                                                                                            2000GB-0024263.
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                                                                              Chen W, Rank DR;
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Pred. No. 1.5;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 469 BP; 125 A; 159 C; 88 G; 97 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAI02735 standard; DNA; 469 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #2726 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI02735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CAGACAGAAGCAGAGATTGAGTGGGGGGGGTGCTGGGTTGCTTGGAGGACAAGTGGCAAGTC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157270-A2
The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe measuring human stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases, with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2001; 2001WO-US00661
                                                                                                                                                                                                                                                  Penn SG,
                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC.
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000;
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                                                                                                                                         Claim 25; SEQ ID No 2726; 322pp; English
                                                                                                                                                                                    Novel single exon nucleic acid probe used to measuring gene expression
                                                                                                                                                                                                                   WPI; 2001-476286/51
                                                                                                                                                                       in a human breast .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgcatttggtgatccggttctgcttccggta 188
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                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2000US-0207456.

2000US-0608408.

2000US-0632366.

2000US-0234687.
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59.3%;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 469 BP; 125 A; 159 C; 88 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe #8769 for gene expression analysis in human cervical cell sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe; human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 cgcatttggtgatccggttctgcttccggta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 CAGACAGAAGCAGAGATTGAGTGGGGGGGGCTGCTGGTTGCTTGGAGGACAAGTGGCAAGTC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                          from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a manual derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO specification, but was obtained in electronic format directly from WIPO specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-2000;
                                                                                                                                                                                                                        analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                           WPI; 2001-488901/53.
                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                      21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-2000;
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                                                                                                                                                          The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                           Claim 25; SEQ ID No 8769; 487pp; English.
                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                            The present sequence is one such probe. The SENPs are derived man HeLa cells. The SENPs can be used to produce a single exon
                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0207456.
2000US-0608408.
2000US-0632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US00670
                                                                                                                                                                                                                                                                                                                                                                          2000GB-0024263
                                                                                                                                                                                                                                                                                                                                                                                          2000US-0234687
2000US-0236359
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                                                                                                                                                                                                                                                                                                               Chen W, Rank DR;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 469;
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B
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Best Local :
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AAI43958/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                           Sequence 542 BP; 150 A; 153 C; 121 G; 118 T; 0 other;
                                                                                                                              The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                              Human genome-derived \sin \dot{\dot{q}}_1 exon nucleic acid probes useful for analyzing gene expression in human placenta -
278 CAGACAGAAGCAGAGATTGAGŢĠGGGGTGCTGTGGTTGCTTGGAGGACAAGTGGCAAGTC 219
                                                                                                                                                                                                           Claim 25; SEQ ID No 12644; 654pp; English.
                                                                                                                                                                                                                                                                           WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                               21-SEP-2000;
27-SEP-2000;
               04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001WO-US00663.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe #12644 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI43958 standard; DNA; 542 BP
                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 542 BP; 150 A; 153 C; 121 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 cgcatttggtgatccggttctgcttccggta 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 CAGACAGAAGCAGAGATTGANTGGGGGGTGCTGGTTGGTTGGAGGACAAGTGGCAAGTC 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 cagacagtggctacggctcagtttgggttgtgctgttgctgggcggcggcgatgacgcctgta 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
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                                                                                                                                                                                                                                                                                                  Hanzel DK,
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                             2000US-0608408
2000US-0632366
2000US-0234687
2000US-0234687
2000US-0236359
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                                                                  3.4%;
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59.38;
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                                                                 Score 31.8;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                 Rank DR;
                                                     Mismatches
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Pred. No. 1.6;
                                                                         DB 22; Length 542;
                                                   37; Indels
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AAF58252/c
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                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
489 tacccaattttattcaataagtcaatatcatgccgttaatatgttgccatccgtggcaat 548
                                                                                                                                                                                                                                                                                                                                                Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other:
                                         429 cgccgcctcttttcatctcactaccacaacgagcgaaltaacccatcgttgagtcaaatt 488
                                                                                                 369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428
                                                                                                                                                        309 aggctctaactattacctgcgaactgtttcgggattgcattttgcagacctctctgcctg 368
                                                                                                                                                                                                                                         249 attatogactoaatgotottacotgttgtgcagatataaaaaatcocgaaacogttatgo 308
                                                                                                                                                                                                                Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-159728/16
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                                                                                                                                                                                                                                                                                   Local Similarity 1.7%; hes 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene expression; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF58252 standard; DNA; 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 AAACTTGGGTGTTCTGGGAAGGCTTCCTGGA 188
                                                                                                                                                                                                                                                                             Conservative 196; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0145695
                                                                                                                                                                                                                                                                                           3.4%; Score 31.8;
1.7%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                         153; Indels
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AAF58254/c
ID AAF582
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Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                      The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 catgctgctaacgtgt@accgcattcaaaatgttgtctgcgattgactcttcttt 603
                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-159728/16.
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                                                                                                                                                                                                                                                                                                                                                                                                         a single surface
                                                                                                                                                                                                                                                               Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
                                                                                                 554 иншининшиншиншийшиншийныншиншишшишшишшишшишшишшишшишш 495
                                                                                                                                                  249 attatogactoaatgotottacotgttgtgcagatalaaaaaatcccgaaaccgttatgc 308
434 ЫММИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИМИТАЛССИМИМИМИМИМИМИМИМИ 375
                                                 369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428
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                     cgccgcctcttttcatctcactaccaccacgagcgaattaacccatcgttgagtcaaatt 488
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                       Conservative 196; Mismatches 153;
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                                                                                                                                                                                                                   3.4%;
                                                                                                                                                                                                                   Score 31.8;
Pred. No. 2.1;
                                                                                                                                                                                                                                  DB 22; Length 936;
                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           549 catgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttcttt 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         489 tacccaattttattcaataagtcaatatcatgccgttaatatgttgccatccgtggcaat 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-159728/16.
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                                                                                                                                                                                                                                                                                                             Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
                                                                                                                                                                                                                                                                                                                                               monitoring gene expression.
                                                                                                                                                                   249 attatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgttatgc 308
                                                                                                       309 aggctctaactattacctgcgaactgtttcgggattgcatttttgcagacctctctgcctg 368
      429 cgccgcctcttttcatctcactaccacaacgagcgaattaacccatcgttgagtcaaatt 488
                                       369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428
                                                                                                                                                                                                                                             Match 3.4%;
Local Similarity 1.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0145695
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                                                                                                                                                                                                                                                      Score 31.8;
Pred. No. 2.1
 DB 22;
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RESULT 14
AAF58259/c
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Sequence 936 BP; 6 A; 138 G; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                                        acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                     369 cgatggttggagttccagacgatacgtogaagtgaccaactaggcggaatcggtagtaag 428
                                                  The present invention relates to a composition comprising two nucleic
                                                                                                   monitoring gene expression.
                                                                                                                           249 attatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgttatgc 308
                                                                                                                                                                                                                                                                                                                                          Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide D2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF58259 standard; DNA; 936 BP
                                                                                                                                                               3.4%; Score 31.8; Local Similarity 1.7%; Pred No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression; ss
                                                                                                                                                         Conservative 196; Mismatches 153; Indels
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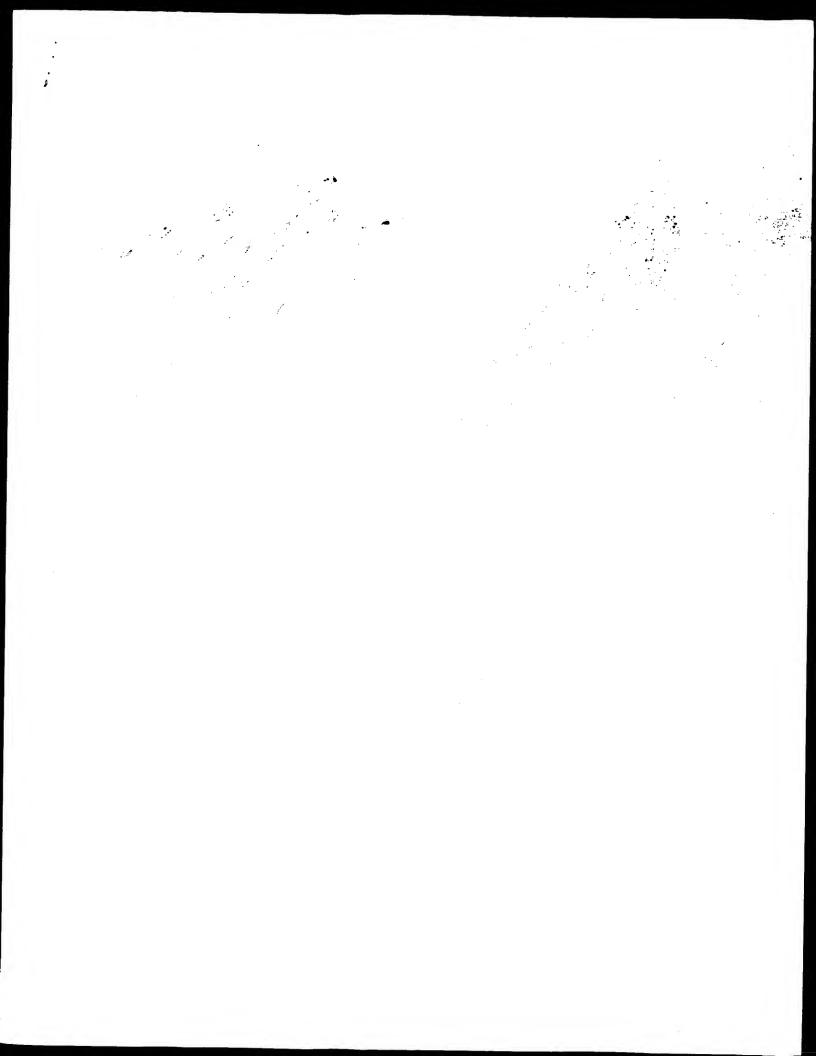
Qγ

369 cgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaag 428

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                                                                                                                                                                                                                                                                                                           The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                                                                                                                                                          Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;
309 aggetetaaetattaeetgegaaetgtttegggattgeattttgeagaeetetetgeetg 368
                                                                             249 attatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgttatgc 308
                                                                                                                                                                                                                                                                                                      monitoring gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 6; Page 128; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses or a single surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-1999;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2000; 2000WO-US20476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electron-transfer group; ETM; mismatch; genotyping;
gene expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF58262 standard; DNA; 936 BP
                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200107665-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0190259
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                                                                                                                                                                                                   DB 22; Length 936;
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548	489 tacccaattttattcaataagtcaatatcatgccgttaatatgttgccatccgtggcaat 548	489	Qy	
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Search completed: January 8, 2002, 17:29:38 Job time: 12758 sec



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OM nucleic - nucleic search, using s\dot{\mathbf{v}} model
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Maximum Match 100%
Listing first 45 summaries
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1 aaacggcaggaggttgttag......cttcaagctgcccctgcagg 934
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                                                                                                                                  351203 seqs, 113238999 residues
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Issued_Patents_NA:*
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Database :

SUMMARIES

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Sequence 13, Appli sequence 1, Appli sequence 7, Appli sequence 7, Appli sequence 17, Appli sequence 17, Appli sequence 112, Appli sequence 114, Appli sequence 114, Appli sequence 1, Appli sequence 114, Appli	- !

Query Match Best Local Similarity 100.0%; Pred. No. 0; Indels 0; G Matches 934; Conservative 0; Mismatches 0; Indels 0; G 1 anacggcaggaggttgttaggcgacctcctgccacccgctttcacgaaggtcatgtgtaggtgtlililililililililililililililililil	US-09-470-618-13 US-09-470-618-13 US-09-470-618-13 Sequence 13, Application US/09470618 Sequence 13, Application US/09470618 Sequence 13, Application US/09470618 GENERAL INFORMATION: APPLICANT: COLOSI, Peter C. APPLICANT: COLOSI, Peter C. APPLICANT: COLOSI, Peter C. ITILE OF INVENTION: Adeno-Associated Vectors for Expresence: APPLICANTON: By Target Cells FILE REFERENCE: AV19en-04082 FILE REFERENCE: AV19en-04082 CURRENT FILING DATE: 1999-12-22 CURRENT FILING DATE: 1999-07-30 EARLIER APPLICATION NUMBER: 60/125,974 EARLIER APPLICATION NUMBER: 60/104,994 EARLIER APPLICATION NUMBER: 60/104,994 EARLIER APPLICATION NUMBER: 00/104,994 EARLIER APPLICATION NUMBER: 00/105,974 EARLIER	C 28 28.6 3.1 1955 2 US-08-478-373-114 C 29 28.6 3.1 1955 3 US-08-478-571-114 C 30 28.6 3.1 1955 4 US-08-8897-704N-1 C 31 28.6 3.1 1955 4 US-08-882-704N-1 28.4 3.0 742 2 US-08-882-704N-2 34 28.4 3.0 4403765 4 US-09-103-840N-2 35 28.4 3.0 441529 4 US-09-103-840N-2 36 28.4 3.0 441529 4 US-08-105-483-87 37 28 3.0 1142 1 US-08-709-209-87 38 30 1142 1 US-08-709-103-87 38 3.0 1142 1 US-08-709-103-87 39 28 3.0 1142 1 US-08-709-103-87 C 40 28 3.0 2696 1 US-08-21-798-1 C 41 28 3.0 2696 1 US-08-21-784-1 C 42 28 3.0 3068 1 US-08-910-584-1 C 43 28 3.0 3068 1 US-08-933-3 C 44 28 3.0 3068 1 US-08-950-720A-7 45 27.8 3.0 405 3 US-08-950-720A-7
Indels 0; Gaps 0 cacgaaggtcatgtgta 60 callillillillillillillillillillillillilli	Expression of Factor VIII	sequence 114, App sequence 114, App sequence 114, App sequence 114, App sequence 114, Appli sequence 1, Appli sequence 2, Appli sequence 87, Appli sequence 87, Appli sequence 87, Appli sequence 1, Appli sequence 3, Appli sequence 7, Appli

0;

T. S.

US-09-364-862-13

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CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/1
EARLIER APPLICATION NUMBER: 60/1
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-364-862-13
                                                                                                                SEQ ID NO 13
                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Couto, Linda B.
APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: CELLS 1.
FILE REFERENCE: AVIGEN-03743:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 11900 tgccttagtatttccttcaagctgcccctgcagg 11933
                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/09364862 Patent No. 6221349
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
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                                               ORGANISM: Artificial Sequence
                                                                               TYPE: DNA
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                                                                                                            11780 tyttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgcccccgg 11839
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                                                                                                                                                                                                                                    11660 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 11719
                901 tgccttagtatttccttcaagctgcccctgcagg 934
                                                                                                                                                                                                                                                                                               11600 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 11659
                                                                841 cgtcgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctt 900
                                                                                                                                                                                                                                                                                                                                                             11540 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 11599
                                                                                                                                                                                                                                                                                                                                                                                                                        11480 gtcaaatttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 11539
                                                                                                                         781 tgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcatcttgccccgg 840
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                                                                                                                                                                                        721 tgaatagocgacgcctttgcatcttccgcactctttctcgacaactctcccccacagctc 780
                                                                                                                                                                                                                                                    661 ttgggtaaggtttgggattagcatcgtcacagcgcgatatgctgcgcttgctggcatcct 720
                                                                                                                                                                                                                                                                                                                 601 tttgtggcattgcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtggg 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11300 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 11359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11240 tottcacgattatcgactcaatgctottacctgttgtgcagatataaaaaatcccgaaac 11299
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                                                                                                                                                                                                                                                                                                                                                                            541 gtggcaatcatgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttc 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                        481 gtcaaattttacccaattttattcaataagtcaatatcatgccgttaatatgttgccatcc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11120 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 11179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11000 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 11059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 totgootgogatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 cgttatgcaggctctaactattacctgcgaactgtttcgggattgcattttgcagacctc 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 tottoacgattatogactcaatgotottacotgttgtgcagatataaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 ttccggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 tgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 aaaggocgcagcgtaactattactaatgaattcaggacagacagtggctacggctcagtt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 aaacggcaggaggttgttagcgcgacctcctgccacccgctttcacgaaggtcatgtgta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y Match 100.0%; Score 934; Local Similarity 100.0%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 11933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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Med Jan 9 14:38:17 2002
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 14 Application US/08232463 sequence 15570367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFUNDANCE, F.

APPLICANT: SCHEIFLINGER, F.

APPLICANT: FALKNER, F.COMBINANT FOMLPOX VIRUS
APPLICANT: FALKNER, F.COMBINANT FOMLPOX APPLICANT INVENTION: 52

TITLE OF SEQUENCES; 52

TITLE OF SEQUENCES Lardner
NUMBER OF SEQUENCES Lardner
NUMBER OF SEQUENCE ADDRESSEE: FOOLEY & LARDNESSEE: ADDRESSEE: 100 Diagonal Road, Suite 500

ADDRESSEE: 100 Diagonal Road, Suite 500

STREET: 100 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: 01.6 (COMPUTER READABLE FLORE) PLOPS WELLING TYPE BM PC COMPUTER: TENDOS WS-DOS WS-DOS COMPUTERS: PSTEM: PC-DOS WS-DOS WS-DOS PRIVARE: PARTY Release #1.0; Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSITICATION: 435
CLASSITICATION DATA:
CLASSITICATION NUMBER:
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: PTZ9Pt-F15
CLONE: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DALE NUMBER 29.768
APPLICADATE: TROPARATION:
FILING AGENT STEPHER 29.768
ATTORNEY BENT, STEPHER 29.768
ATTORNEY BENT, STEPHER: 3047:
REGISTRATION INFORMATION:
REFERENCE TOTON INFORMATION:
REFERENCE (7/03)835-9300
TELECOMMUNICATION 100

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           4.0%; Score 37.6; DB 1; Length 7; Onery Match Similarity 2.7%; pred. Mismatches 101; Indels Best Local 7; Conservative 152; Mismatches Matches
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TYPE: nucleic acid
TYPE: STRANDEDNESS: SINGLE
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                   670 grtt999atragcatcgtcacagcgcgatatgctgcgcttgcttggatcgttgaatagcc 729
                                                                                                                                                                                                                                         730 gacgootttgcatottccgcatttttctcgacaactctcccccacagctctgttttggc 789
                                                                                                                                                       790 aatatoaaccycacgycctytaccatgycaatctctgcatcttgcccccggcgtcgcggc
                                                                            850 actacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctttgccttagt 909
1298 YYYYYYYYYYYYYYYYY 1317
                                      910 attroctromagorgococt 929
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GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: Pett, Karen A.

APPLICANT: OLSON, Antisense

APPLICANT: NUMBER: US/09/045,301A

ATTLE OF FRENCE: 10498/03-20

CURRENT APPLICATION NUMBER: 60/041182

CURRENT APPLICATION NUMBER: 60/041182

CURRENT APPLICATION NUMBER: 1998-03-21

EARLIER FILING DATE: 1997-03-21

EARLIER FILING DATE: 197-03-21

EARLIER FILING DATE: 197-03-21

SOFTMARE: Patentin Ver. 2.0
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NAME/KEY: (1809)...(2252)
LOCATION: (1809)...
100-09-045-301-1
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Best Local Si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-195-868-11/C
US-09-195-868-11/C
Sequence 11 6090671
Sequence 11 6090671
Sequence 11 6090671
Sequence 11 6090671
Sequence 11 Neormary No. MICHAEL
SEQUENCE STOLEMENT FOR PH.D. MOPHD, LEWIS T.
APPLICANT: WILLIAMS SIGNALING
APPLICANT: WILLIAMS

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US-09-195-868-11/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                378 gagttccagacgatacgtcgaagtgaccaactaggcggaatcggtagtaagcgccgctc 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4525 gacctgccgarggtactggcacctgagcaattcctagtccttrttggtctgggcctc 4584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 tettoatotoactacoacaacgagogaattaacccatogttgagtcaaatttacccaatt 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4668
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                                                                                                                                                                                                                                                                                               ZIP: WADUB ABLE FORM: 15K
COMPUTER READABLE FORMS DOS
MEDIUM TYPE: HA PC CC-DOS/MS-DOS
ORDERING SYSTEM: Release #1.0, Version #1.30
CORRENT OF PACENTIN RALEASE #1.0, VERSION APPLICATION DATA:
SOFTWARE: PACENTIN BATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE 4560 HORTON STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: EMERYVILLE
                                                                                                                                                                           CLASSIFICATION: US/09/195,868
CLASSIFICATION NUMBER: US/09/195,868
APPLICATION NUMBER: US/09/195,868
APTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT
                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 31.6; DB 4; Length 4:
Score 31.6; DB 4; Indels
Pred. No. 1.4; 59; Indels
O; Mismarches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 4668;
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ATELLING DATE:
ANAMEN/AGENT INFORMATION:
REGISTRATION NUMBER: 36.
REGISTRATION NUMBER: 36.
REFERENCE/COCKET NUMBER: 36.
TELEPHONE: 510 INFORMATION:
TELEPHONE: 510 INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 3691 base Peairs
TOPALOGY: 110ar
MOLECULE TYPE: 110ar
MOLECULE TYPE: CDNA
                                                                                                                                                                                                             CURENT APPLICATION PALE
APPLICATION NATION DATA:
FILING DATE: US/
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: E FORM:
COMPUTER: ELOPPY disk
OPERATING SYSTEM: ECOMPALIBLE
SOFFWARE: PATANTIN BAJANES MINO
                                                                                                                                                                        APPLICATION NUMBER: US/09/195,868
                                                                                                                                                                                                                                                                                                                          APPLICANT: KAYANANGH MD. MICHAEL
TITLE OF INVENTION: S-PHOSPHATION: APPLICANT: HOT PH.D. DAVID
TITLE OF INVENTION: S-PHOSPHATASES (SIPS)
ADDRESSENCE ADDRESS: 3
STREET: 4560 HORTON STREET
CATTE: CATYULLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
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Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FIRESTONE, LEIGH H.
REGISTRATION NUMBER: 36.8.1
TELECOMMUNICATION NUMBER: 36.8.1
TELEPHONE: 510-92-32707
INFORMATION FOR SEQ 13.5.2
LENGTH: 2940 base pairs: 578AWESSES: 3114
TYPE: INCOLE 12.6.114
TYPE: 1.0.124
MOLECULE TYPE: LINEAR
MOLECULE TYPE: LINEAR
US-09-195-868-11 CDNA
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL
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1581 ATAGCACC 1574
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Best Local Similarity 3.38; Score 31.2;
Matches 45; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1641 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTTCTGGGACTTGGTCTTCAATGTGGC 1582
                                                                                                                                                                                                                                                                                                      94608
RE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2, Application US/09195868
                                                                                                                                                                                                            Release #1.0, Version #1.30
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                                                                                                                   1182.004
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1588 ATAGCACC 1581

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US-09-418-540-1/c
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                                                                                                                                                                                                                                                                                                                                                                                    US-09-418-540-1
               US-08-664-962B-7/c
Sequence 7, Application US/08664962B
Patent No. 6218162
GENERAL INFORMATION:
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APPLICANT: Pot, D
                                                                                                                                                                                                                                                                                                          Query Match 3.3%;
Best Local Similarity 66.2%;
                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Williams, Lewis T.
APPLICANT: Jefforson, Anne Bennett
APPLICANT: Majorus, Philip W.
APPLICANT: Molegan No. 6296848el Grb2 Associating Protein and Nucleic TITLE OF INVENTION: Acids Encoding Therefor NUMBER OF SEQUENCES: 10 ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/418,5%0
FILING DATE: 14-OCT 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 17-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: Q6: 08/560,005
FILING DATE: 17-NOV-1595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 4147 base pairs
TYPE: nucleic acid .
STRANDEDNESS: single
                                                                                                                                                                                                                   1648 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTCTGGGACTTGGTCTTCAATGTGGC 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             1588 ATAGCACC 1581
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APPLICANT: Krystal, Gerald
                                                                                                                                                                                                                                         549 catgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttctttgtggc 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Dow, Karen B. 29,684 REGISTRATION NUMBER: 29,684 REFERENCE/DOCKET NUMBER: 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                609 attgcacc 616
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                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                              45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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17..2944
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 Mismatches

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                                                                                                                                                                                                                                                                                                                    Score 31.2; D
Pred. No. 1.9;
                                                                                                                                                                                                                                                                                                                                       DB 4; Length 4147;
                                                                                                                                                                                                                                                                                                        23; Indels
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US-08-664-962B-7
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                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                               Sequence 7, Application US/09311743

Patent NO. 6238903

GENERAL INFORMATION:
APPLICANT: KTYSTAI, Gerald
APPLICANT: KTYSTAI, Gerald
TITLE OF INVENTION: SH2-CONTAINING INOSITOL-PHOSPHATASE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SH2-CONTAINING INOSTTOL-PHOSPHATASE NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 4870 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                  2377 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTCTGGGACTTGGTCTTCAATGTGGC 2318
                                                                                                                                                                                                                                                                                                                                     2317 ATAGCACC 2310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mueller, Douglas P. REGISTRATION NUMBER: 30,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 14-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  549 catgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttctttgtggc 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   609 attgcacc 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.3%;
Local Similarity 66.2%;
les 45; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
COUNTRY: Canada
ZIP: M5H 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55402-4131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3100 No. 6218162west Center, 90 South Seventh Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hSHIP
                                                                                  STREET: 40 King Street West
CITY: Toronto
STATE: Ontario
                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
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                                                                                                                                       BERESKIN & PARR
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US-09-007-005-17

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APPLICANT: EXOSTAK, Jack W.
APPLICANT: ROSETAK, RICHARD W.
APPLICANT: LIU, RIHE
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: 03/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/05/963
EARLIER FILING DATE: 1997-01-37
EARLIER FILING DATE: 1997-01-37
EARLIER FILING DATE: 1997-01-06
NUMBER OF SEQ ID NOS: 33
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Sequence 17, Application US/09007005B

Patent No. 6258558
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                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
OTHER INFORMATION: n = A,T,C or G
                  NAME/KEY: misc_feature LOCATION: (1)...(289)
                                                                OTHER INFORMATION: Translation template
                                                                                                       ORGANISM: Artificial Sequence
                                                              FEATURE:
                                                                                                   FEATURE:
                                                                                                                                       TYPE: RNA
                                                                                                                                                         ENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2377 CAAGCAGCTCGAGTGGAACTCCAGGTAGAATTTGGTCTGGGACTTGGTCTTCAATGTGGC 2318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2317 ATAGCACC 2310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             609 attgcacc 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 catgctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttctttgtggc 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, #icheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens IMMEDIATE SOURCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE: hSHIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 416-361-1398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/311,743 FILING DATE: 14-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 416-364-7311
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Pred. No 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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: LOCATION: (1)...(289)
: OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-244-796-17/c
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                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 5.7%; Pred. No. 0.45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/09244796 Patent No. 6281344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN TITLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Liu, Rihe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 13; Conservative
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Best Local Similarity 5.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Roberts,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Szostak, Jack W
127 YNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS 68
                                         825 tycatcttycccccggcytcgcggcactacggcaataatccgcataagcgaatgttgcga 884
                                                                                           187 YNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS 128
                                                                                                                                     765 ctctcccccacagctctgttttggcaatatcaaccgcacggcctgtaccatggcaatctc 824
                                                                                                                                                                                      247 YGYAYGYTYTYAYCYGYCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYS 188
                                                                                                                                                                                                                              705 egettgetggeateettgaatageegaegeetttgeatetteegeaetetttetegaeaa 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  885 gcacttgcagtacctttgccttagtatttccttcaagctgcccctgc 931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825 tgcatcttgcccccggcgtcgcggcactacggcaataatccgcataagcgaatgttgcga 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               765 ctctcccccacagctctgttttggcaatatcaaccgcacggcctgtaccatggcaatctc 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 egettgetggeateettgaatageegaegeetttgeatetteegeaetetttetegaeaa 764
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                                                                                                                                                                                                                                                                                                13; Conservative
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                                                                                                                                                                                                                                                                                 95; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Score 31; DB 4; Length 289; Pred. No. 0.45; 95; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                Matches
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: .112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 01
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-19#3
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         REGISTRALLON NOT NUMBER: 1038
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                FEATURE:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                             837 ccggcgtcgcggcactacggcaataatccgcataagcgaatgttgc 882
                                                                                  777 getetgttttggcaatateaacegcaeggcetgtaccatggcaatetetgcatettgccc 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
925 CTAGTTCTTCAGCATTAGGCCCCATAAAAACCACCTTCTAATGTTCC 880
                                                             APPLICATION NUMBER: US/08/487,890A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                            / Match 3.3%;
Local Similarity 55.7%;
les 59; Conservative
                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                             nucleic acid
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Schryvers, Anthony
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                                                                                                                         0; Pred. No. 1.6;
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                                                                                                                                                               score 30.8; DB 1; Length 1951;
                                                                                                                                        47; Indels
                                                                                                                                            0; Gaps
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0;

Gaps

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RESULT 14
US-08-478-435-112/c
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В
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                                                                                                                   Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 595-11
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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925 CTAGTTCTTCAGCATTAGGCCCATAAAAACCACCTTCTAATGTTCC 880
                          837 ccggcgtcgcggcactacggcaataatccgcataagcgaatgttgc 882
                                                                        777 getetgttttggcaatateaacegeaceggcetgtaccatggcaatetetgcatettgccc 836
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                                                        APPLICATION NUMBER:
                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael REGISTRATION NUMBER: 24
                                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                / Match 3.3%; Score 30.8; DI
Local Similarity 55.7%; Pred. No. 1.6;
nes 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                  TYPE:
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                                                                                                                                                                                                                                                                                               LENGTH:
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Klein, Michel
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Yang, Yan-Ping
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Schryvers, Antho
                                                                                                                                                                                                                                                                                                  1951 base pairs
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                                                                                                                                                                                                          1..1890
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                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                           (416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER: US 08/337,483
08-NOV-1994
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                                                                                                                                                                                                                                                                                                                                              595-1163
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                                                                                                                                                      DB 2; Length 1951;
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Search completed: January 8, 2002, 17:21:33 Job time: 12344 sec
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; LOCATION:
US-08-337-483-112
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/337,483
FILING DATE: 08-NOW-1994
CLASSIFICATION: 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-08-337-483-112/c
                                                                                                                                                                                                                                  Query Match 3.3%; Score 30.8; DB 2; Length 1951; Best Local Similarity 55.7%; Pred. No. 1.6; Matches 59; Conservative 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 112, Application US/08337483 Patent No. 5922562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION UNMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION: 416) 595-1155
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 112:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1951 base pairs
TYPE: nucleic acid
                                                                              925 CTAGTTCTTCAGCATTAGGCCCATAAAAACCACCTTCTAATGTTCC 880
                                                                                                     837 ccggcgtcgcggcactacggcaataatccgcataagcgaatgttgc 882
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APPLICANT:
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CORRESPONDENCE ADDRESS: Sim & MCBurney
STREET: Suite 701, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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Yang, Yan-Ping
Murdin, Andrew
Klein, Michel
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Harkness, Robin
Schryvers, Anthony
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OM nucleic - nucleic search, using sw model
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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934
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gb_est1:*
                                                   em_gss_hum: *
em_gss_inv: *
em_gss_pln: *
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gb_htc: *
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em_gss_fun: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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387.2 380.2	522.2 455.4 454.2 420.6	588 569.6 531.4	Score 724.4
41.5 41.5 40.7	448.8 45.0	63.0 61.0 56.9	Query Match I
688 775	714 743 500 617	546 646	Query Query Match Length DB 77.6 734 1
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11 BI269141 10 AV404200	AV404019 BE420137 AV403989 BF328036	BG451667 AI489217 AW624097	D D AV404408 AV65168
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6.6	7.2	7.9	8.9	8.9	ω. ω	9.3	10.1	11.8	12.5	13.0	13.5	13.7	16.5	18.7	19.7	23.0	23.3	24.3	26.3	27.9	30.3	30.7	31.5	31.5	31.9	32.7	33.9	35.0	36.2	38.5	39.8	9.9	>
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B1269244	B1263664	CNSOLITE	BGU53849	BG102333	BG451510	AWU38U61	BE038061	B1190428	BF-65/6/5	CVVV00	C221/0	A1490216	A18983/0	AV404308	BG312975	BF634207	BF934675	B1208/80	BG459413	N84801	BE456/9/	B1260410	B1200033	BI268/8/	AW619942	B128709	B1268701	BE303471	BE45444	AV/49420	AA8413/9	1111	BC312470
-	NF005H10		AI.147672 Anopheles	BC053849 RHIZ2 10	BG102333 RHIZ2 22	z 1		BF552927 UI-R-C2-n	i 1d1	BF657675 OV2 20 D0	C22255 Miva	2175	ATA90216 EST248542	ATRO8370 EST267813	AVADA 308 AVADA 308		BE634207 NE074G04D	BF934675 RC4-NT100	BT268786 NF015B02G	BG459413 M79B19STM				BI268699 NF023B06G						3/// PST4055	AV749428	MB3D6AA9	BG312470 WHE2408_F

ALIGNMENTS

RESULT

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,	FEATURES Source		AUTHORS TITLE JOURNAL COMMENT	ISM S	AV404408 LOCUS DEFINITION ACCESSION VERSION
/organism="Bombyx mori" /strain="Shuko x Ryuhaku" /db_xref="taxon:7091" /clone="pg0946" /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult"	(5' -> 3') (5' -> 3') Project='Silkworm Genome Program in MAFF, and Research for the Projectan in JSPS'. see 'SilkBase', Future Program in JSPS'. see 'SilkBase', Ahttp://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb. Location/Qualifiers 1. 734	Genome Research Group National Institute of Radiological Sciences Nanagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@nirs.go.jp method:uni-directional, sequence direction:sequenced from T3 primer	MITA,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S. Bombyx mori cDNA Unpublished (2000) Contact: Mita K	EST. domestic silkworm. domestic silkworm. Bombyx mori Bombyx mori Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Plombycoidea; Bombycidae; Bombyx.	AV404408 734 bp mRNA EST 06-FEB-2000 AV404408 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult Bombyx mori cDNA clone pg0946 T3, mRNA sequence. AV404408 AV404408.1 GI:6908496

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KEYWORDS
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                                                                                                                                                                                                                            CCCCACAGCTCTGTTTTGGCAATATCAACCGCACGGCCTGTACCATGGCAATCTCTGCAT
                                                                                                                                                                                                                                         ccccacagetetgttttggcaatateaäcegeaeggeetgtaeeatggeaatetetgeat 829
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                                AI065168 628 bp mRNA
ESTTRKA-8 Rat Lambda Zap II Library, Stratagene #936501 Rattus
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/tissue_type="pheromone gland"
/dev_stage="newly-eclosed adul:
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                                                                                       612 gcaccaccagagcgtcatacagcggcttaacagtgcgtgaccaggtgggttgggttaggt
                                                                  208 GCACCACCAGAGCGTCATACAGCGGCTTAACAGTGCGTGACCAGGTGGGTTGGGTAAGGT 149
                                                                                                                                       268 GCTGCTAACGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTCTTTGTGGCATT
                                                                                                                                                          552 gctgctaacgtgtgaccgcattcaaaatgttgtctgcgattgactcttctttgtgggcatt 611
                                                                                                                                                                                                            328 CCAATTTTATTCAATAAGTCAATATCATGCCGTTAATATGTTGCCATCCGTGGCAATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: huangbr@cdm.imicams.ac.cn
Seq primer: M13 Forward Primer.
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/dev_stage="6 weeks"
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/db_xref="taxon:10116"
/clone="pGEM-T/TRKA-8MF"
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Pred. No. 1.5e-174;
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                                                                                                                                                         ggaaagagcactggctaaccaggctcgccgactcttcacgattatcgactcaatgctctt 268
                                                                                                                                                                                                                                                               Medicago truncatula Medicago; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; endicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.; Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG451667.1 GI:1337,0461
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The Samuel Roberts Noble Foundation
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/tissu@_type="plantlets"
/tissu@_type="pooled timepoints"
/dev_stage="pooled timepoints"
/note="wector: Lambda Zap; Contains a mixture of entile the contains a mixture of entile the contains a mixture of entile contains a mixtu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        389 gətacytcqaaytgaccaactagycygaatcygtagtaaycygccycctttttcatctca 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST247556 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
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AI489217
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                                                                                                                                                                                                                                                                                                                                                                  100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.L., Nierman, W., Fras, S.D. and Giovannoni, J.
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                                                                                     166
                                                                                                                 /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: xho1; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5' and 3' ends located at the EcoRI and XhoI sites,
                                                                                                  respectively."
                                                                                                                                                                                     /tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF/"
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/clone="cLED17L7"
                                                                                                                                                                                                                                                                                                                  /organism="Lycopersicon esculentum
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Score 569.6; DB 10 Pred. No. 1.1e-163;
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                      Length 656;
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Query Match

Best Local Similarity

61.0%;

DB 10;

Matches

572;

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REFERENCE
AUTHORS
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                                                                                     Email:
                                                                                                                            Clemson University Genomics Institute
                                                                                                                                                                        van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and Tanksley,S.D. Generation of ESTs from tomato flower tissue, 3-8 mm buds
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                                                                                                                                                     Contact: CUGI
                                                                                                                                                                   Unpublished (1999)
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Lycopersicon esculentum cDNA clone cTOB14J1 5', mRNA sequence
                                                              mail: http://www.genome.clemson.edu/orders/index.html
prime sequence.
                                                                                                                                                                                                                                                      (bases 1 to 546)
                                                                                              Jordan Hall, Clemson,
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/cultivar="TA496"
                                              Location Qualifiers
        /organism="Lycopersicon esculentum"
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                                                                                                                                                                                                                        Holt, I.E., Liang
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                                                                                                                                                                                                                                                                                                      604 gtggc 608
                                                                                                                                                                                                                                                                                                                                               545 caatcatgctgctaac-gtgtgaccgcattcaaaatgttgtctgcgattgactcttcttt
                                                                                                                                                                                                                                                                                                                                                                                              425 taagegeegeetetttteateteactaceacaaegagegaattaaeceategttgagtea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 TAAGCGCCGCCTCTTTTCATCTCACTACCACCACGAGCGAATTAACCCATCGTTGAGTCA
                                                                                                                                                                                                                                                                                                                               65 CAATCATGCTGACGGTGTGACCGCATTCAAAATGTTGTCTGCGATTGACTCTTCTTT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGCAGGCTCTAACTATTACCTGCGAACTGTTTCGGGATTGCATTTTGCAGACCTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCGATGGTTGGAGTTCCAGACGATACGTCGAAGTGACCAACTAGGCGGAATCGGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cacgattatcgactcaatgctcttacctgttgtgcagatataaaaaatcccgaaaccgtt 304
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                                                                  Bombyx mori
                                                                                domestic silkworm.
                                                                                                                 AV404019.1 GI:6908107
                                                                                                                                      AV404019 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult Bombyx mori cDNA clone pg--0345 T3, mRNA sequence.
                                                                                                                                                                                       AV404019
(bases 1 to 714)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Clone_lib="tomato flower buds 3-8 mm, Cornell University"
/tissue_type="flower"
/dev_stage="3-8mm buds"
/note="Vector: pBBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol: supplier: Tanksley; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
a 124 c 135 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="cTOB14J1"
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                                                                                                                                                                                 714 bp
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99.6%;
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                                                                                                                                                                                   mRNA
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LOCUS BE420137 743 bp mRNA EST 24-JUL-2000 DEFINITION WWS020.E9R000101 ITEC WWS Wheat Scutellum Library Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 gcgaattaacccatcgttgagtcaaatttacccaattttattcaataagtcaatatcatg 520
                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                       641 acagtgcgtgaccaggtgggttgggtaaggtttgggattagcatcgtcacagcgcgcgatat 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GCGAATTAACCCATCGTTGAGTCAAATTTACCCCAATTTTATTCAATAAGTCAATATCATG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 55.9%;
Local Similarity 99.2%;
                                                                                                                                                               1 TGACCAACTAGGCGGAATCGGTAGTNAGCGCCGCCTCTTTTCATCTCACCTACCACAACGA 60
                                                                                                                                 881 gcgagcacttgcagtacctttgccttagtatttccttcaagctgcccc 928
                                                                                                                                                                                                                                                                                                                                                                                                                 TIGICTECCATTGACTCTTTTGTGGCATTGCACCACCAGAGCGTCATACAGCGGCTTA 240
                                                                                                                                                                                                                                                                                         ttgtctgcgattgactcttcttttgtggcattgcaccaccagagcgtcatacagcggctta 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524;
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                                                                                                                                                                                                                             ACAACTCTCCCCCACAGCTCTGTTTTGGCAATATCAACCGCACGGCCTGTACCATGGCAA 420
                                                                                                                                                                                                                                              acaactetececeacagetetgttttggcaatatcaacegcaeggcetgtaceatggcaa 820
                                                                                                                                                                                                                                                                                                                                                    ACAGTGCGTGACCAGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Future program in JSPS'. see 'SilkBase', for whole ESTdb http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                method:uni-directional, Sequence direction:sequenced from T3 primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anagawa 4-9-1, Inage, Cl
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
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                                                                                                 GCGAGCACTTGCAGTACCTTTGCCTTAGTATTTCCTTCAAGCTTTGCC 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project='Silkworm'Genome Program in MAFF, and Research for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"
200 c 158 g 195 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 newly-eclosed adult"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:7091"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Bombyx mori"
/strain="Shuko x Ryuhaku"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="pg--0345"
/clone_lib="Bombyx mori pheromone gland Shuko
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0; Mismatches
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                                                                                                                                                                                                        181
                                                                                                                                                                                                                                        577
757 ctcgacaactetcccccacagctctgttttggcaatatcaaccgcacggcctgtaccatg
                                                                 301 ATATECTECCETTECTECATCCTTCAATAGCCGACGCCTTTCCATCTTCCGCACTCTTT 360
                                                                                                                                    241 CTTAACAGTGCGTGACCAGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                         1 GAAGTGACCAACTAGGCGGAATCGGTAGTAAGGGCCGCCTCTTTTCATCTCACTACCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                           gaagtgaccaactaggcggaatcggtagtaagcgccgcctcttttcatctcactaccaca 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA clone WWS020.E9, mRNA sequence. BE420137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              456;
                                                                                                                                                                                                      AATGTTGTCTGCGATTGACTCTTCTTTGTGGCATTGCACCACCAGAGCGTCATACAGCG
                                                                                                                                                                                                                          aatgttgtctgcgattgactcttctttgtggcattgcaccaccagagcgtcatacagcgg 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Sharifiou, M., Sorrells, M., Warburton, M. and Wenzel, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                   atatgctgcgcttgctggcatccttgaatagccgacgcctttgcatcttccgcactcttt 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zeneca Wheat Improvement Centre, Norwich Research Park
Colney Lane, Norwich NR4 7UH UNITED KINGDOM
Tel: 44 1603 250 2600
Fax: 44 1603 250 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Schuch W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: wolfgang.schuch@aguk.zeneca.com
International Triticeae EST Cooperative (ITEC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Novosibirskaya 67"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="scutellum callus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="ITEC WWS Wheat Scutellum Library"
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reverse sequencing primer used for 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 455.4; DB 10; Length 743; pred. No. 1.3e-128;
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770 ccccacagctctgttttggcaatatcaaccgcacggcctgtaccatggcaatctctgcat 829
                                                    241 GCTGGCATCCTTGAATAGCCGACGCCTTTGCATCTTCCGCACTCTTTCTCGACAACTCTC 300
                                                                   710 gotggcatcottgaatagoogaogcotttgoatottcoggcactotttotogacaactotc 769
                                                                                                                    181 GACCAGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGCGCGATATGCTGCGCTT 240
                                                                                                                                      650 gaccaggtgggttgggtaaggtttgggattagcatcgtcacagcgcggatatgctgcgctt 709
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                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project-'Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS', see 'SilkBase', for whole ESTdb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method:uni-directional, sequence direction:sequenced from T3 primer
(5' -> 3')
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bombyx mori cDNA
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AV403989 500 bp mkNA
AV403989 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed
adult Bombyx mori cDNA clone pg--0306 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domestic silkworm.
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                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="newly-eclosed adult" 141 c 107 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="pheromone gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone="pg--0306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Bombyx mori"
                                                                                                                                                                                                                                                                                                                                                                                                  48.68; Score 454.2; DB 10; Length 500; 99.38; Pred. No. 2.5e-128;
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Matches 456; Best Local Similarity

Conservative

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Mismatches

Indels Length 617;

3; Gaps

45.0%; Score 420.6; DB 11; 98.5%; Pred. No. 5.6e-118;

Query Match

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                                                                                                                                                                                                                                                                    High quality sequence start: 47 High quality sequence stop: 617.
                                                                                                                                                                                                                                                                                            This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.bb/Scripts/gethtml2.pl?tl=QV3&t2=QV3-BN0149-160800-292-g05&t3=2000-08-16&t4=1) Seq primer: puc 18 forward ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-270700J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20202663
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1 (bases 1 to 617)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BF328036 617 bp mRNA EST 22-NOV-2000
QV3-EN0149-160800-292-g05 EN0149 Homo sapiens cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
tissue mRNA and cDNA amplification were performed under low stringency conditions."

152 c 151 g 156 t
                                                /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                        /dev_stage="Adult"
                                                                                                                                                                                /clone_lib="BN0149"
                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 CTCTTCACGATCATCGACTCAATGCTC-TACCTGTTGTGCAGATATAAAAAATCCCGAAA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ttgggttgtgctgttgctgggcggcgatgacgcctgtacgcatttggtgatccggftctg 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 CGGTAGTAAGCGCCCCCCTTTTCATCTCACTACCACACGGCG 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell/C., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula drought library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NF074F11DT1F1094 Drought Medicago truncatula cDNA clone NF074F11DT 5', mRNA sequence.
                                                                                                                                                                                                                                                                     Email: gdmay@noble.org
Insert Length: 685 St
Plate: 074 row: F col
                                                                                                                                                                                                                                                                                                                          2510 Sam Noble Parkway, Ardmore, OK 73402, Tel: 580 221 7391 Fax: 580 221 7380
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The Samuel Roberts Noble Foundation
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primer: TCACACAGGAAACAGCTATGAC
                        163
                        മ
                        timepoints.
                                                         plantlets harvested in a series
                                                                             /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                    /clone_lib="Drought"
                                                                                                                                                                               /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                                         /clone="NF074F11DT"
                                                                                                                                                                           /db_xref="taxon:
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                        169 g
                                                                   of days-post-watering
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                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 44.9%; Score 419.4; DB 11; Length 685; Best Local Similarity 99.8%; Pred. No. 1.4e-117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260 AAACGGCAGGAGGTTGTTAGCGCGACCTCCTGCCACCCGCTTTCACGAAGGTCATGTGTA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 TTCCGGTATTCGCTTAATTCAGCACAACGGAAAGAGCACTGGCTAACCAGGCTCGCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 tgggttgttgctgttgctgggcggcgatgacgcctgtacgcattttggtgatccggttctgc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 TCTTCACGATTATCGACTCAATGCTCTTACCTGTTGTGCAGATATAAAAAATCCCGAAAC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ttcoggtattcgcttaattcagcacaacggaaagagcactggctaaccaggctcgccgac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 tctgcctgcgatggttggagttccagacgatacgtcgaagtgaccaactaggcggaatcg 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tottcacgattatcgactcaatgctcttacctgttgtgcagatataaaaaaatcccgaaac 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGGTTGTGCTGTTGCTGGGCGGCGATGACGCCTGTACGCATTTGGTGATCCGGTTCTGC
                                                                                                                                                                                                                                                                                                           Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF003A05IR1F1036 Irradiated Medicago truncatula cDNA clone NF003A05IR 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        barrel medic.
Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BI269141.1 GI:14875595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI269141
                                                                                                                                                                        The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391 Fax: 580 221 7380
                                                                                                                Email: gdmay@noble.org
Insert Length: 688 Si
Plate: 003 row: A co.
                                                                                                                                                                                                                                                                        Contact: May GD
                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                               Medicago.
                                                                                           Seq primer: TCACACAGGAAACAGCTATGAC
                                                                                                                                                                                                                                                     Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 688)
                  /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                            1. .688
/clone="NF003A05IR'
                                                                          Location/Qualifiers
                                                                                                                    row: A column: 05
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                                                                                                                                       Std Error: 0.00
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 caaaatgttgtctgcgattgactcttctttgtggcattgcaccaccagaggggtcatacag 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 atcatgccgttaatatgttgccatccgtggcaatcatgc-tgctaacgtgtgaccgcatt 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CAAAATGTTGTCTGCGATTGACTCTTCTTTGTGGCATTGCACCACCAGAGCGTCATACAG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATCATGCCGTTAATATGTTGCCATCCGTGGCAATCATGCGTGCTAACGTGTGACCGCATT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATGGCAATCTCTGCATCTTGCCCCCCGGCGTCGCGGCACTACGGCAATAATCCGCATAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGGCTTAACAGTGCGTGAÇCÄGGTGGGTTGGGTAAGGTTTGGGATTAGCATCGTCACAGC
                                         Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,
Bombyx mori cDNA
Unpublished (2000)
                              Contact: Mita K
                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                          AV404200 775 bp mRNA EST 06-FEB-2000 AV404200 Bombyx mori pheromone gland Shuko x Ryuhaku newly-eclosed adult Bombyx mori cDNA clone pg--0693 T3, mRNA sequence.
                                                                                                                                                                                                                                                Bombyx mori
                                                                                                                                                                                                                                                                                                                      AV404200.1 GI:6908288
                                                                                                                                                                                                                                                                      domestic silkworm.
                                                                                                                                      (bases 1 to 775)
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Research Group
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="seedlings"
/dev_stage="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Irradiated"
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98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 387.2; DB 11,
Pred. No. 1e-107;
Pred. No. 1e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  155 g
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                                                                                                                                                                         ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTAGTATTTCCTTCAAGCTTTGCC 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGGCACTACGGCAATAATCCGCATAAGCGAATGTTGCGAGCACTTGCAGTACCTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgcggcactacggcaataatccgcataagcgaatgttgcgagcacttgcagtacctttgc
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Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Dvorak,J., Fenton,R.D., Gustafson,P., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R., Miller,R., Otto,C., Nguyen H.T., Rausch,C.J.
                                                                                                                                                                                                                                                             BG312470 373 bp mRNA EST 23-FEB-2001 WHE2408_F10_L207S Wheat 3-6 DAP seed cDNA library Triticum aestivum cDNA clone WHE2408_F10_L20, mRNA sequence.
                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                      BG312470
BG312470.1 GI:13114273
                                                                                                                                                                                              bread wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        National Institute of Radiological Sciences Anagawa 4-9-1, Inage, Chiba 263-8555, Japan Email: kmita@nirs.go.jp
                                                                                                  Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              method:uni-directional, sequence direction:sequenced from T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Project='Silkworm Genome Program in MAFF, and Research for the
                                                                             (bases 1 to 373)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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newly-eclosed adult"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"
211 c 185 g 218 t
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/db_xref="taxon:7091"
/clone="pg--0693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bombyx mori"
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99.2%;
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                                                                                                          cgaagtgaccaac 408
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                                                                                                                                                                                                                                                     gtgcagatataaaaaatcccggaaaccgttatgcaggctctaacctattacctgcgaactgt 335
                                                                                                                                                                                                                                                                                                                                                                                                                       tacgcatttggtgatccggttctgcttccggtattcgcttaattcagcacaacggaaaga 215
                                                                                                                                                                                                                                                                                                          GCACTGGCTAACCAGGCTCGCCGACTCTTCACGATTATCGACTCAATGCTCTTACCTGTT 240
                                                                                                                                                                                                                                                                                                                                            gcactggctaaccaggctcgccgactcttcacgattatcgactcaatgctcttacctgtt 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAGACAGTGGCTACGGCTCAGTTTGGGTTGTGCTGTTGCTGGGCGGCGATGACGCCTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCGCTTTCACGAAGGTCATGTGTAAAAGGCCGCAGCGTAACTATTACTAATGAATTCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Olin Anderson,
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, GA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Seaton,C.L., Simons,K., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - 3-6 DAP.seed CDNA library
Unpublished (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Uni ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Total RNA was prepared from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Wheat 3-6 DAP seed cDNA library"
/tissue_type="Young seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
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/db_xref="taxon:4565"
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Pred. No. 1.8e-103;
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GCACTGGCTAACCAGGCTCGCCGACTCTTCACGATTATCGACTCAATGCTCTTACCTGTT
                         gcactggctaaccaggctcgccgactcttcacgattatcgactcaatgctcttacctgtt 275
                                                                                                                                                                                                                                                                           gacagacagtggctacggctcagttttgggttgttgctgtttgctgggcggcgatgacgccttg 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Onchocercidae; Brugia.
1 (bases 1 to 498)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mark.blaxter@ed.ac.uk
The ABI trace of this sequence can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +44 131 650 6760 Fax: +44 131 670 5450
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/lab_host="E. coli xL1-Blue"
/note=""Vector: lambdaZapII (UniZap XR); Site_1: Eco R I
(5 'end); Site_2: Xho I (3 'end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNASE H and DNApol I. The library had 2 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Waniewski.
The library is available from The Filarial Genome Project
Resource Center: contact Dr. S.A. Williams, Clark Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center, Smith College, Northampton, MA 01063 USA phone +1 413 585 3826 fax +1 413 585 3786 email genome@smith.edu." 139 c 123 g 134 t
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larvae SAW96MLW-BmL3d6"
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Pred. No. 4.8e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                    Email: mbshi@ms.stn.sh.cn
This clone is available at Shanghai Hematology Institute
                                                                                                                                                                                                                                                                                                                                                                                                                              Shanghai Institute of Endocrinology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han,Z., Chen,Z., Hu,R. and Chen,J. Homo sapiens NPC library cDNA clones Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Song,H., Peng,Y., Ĝu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q., Han,Z., Chen,Z., Hu,R. and Chen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 399)
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AV749428
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Shoujing Road, Zhangjiang
Location/Qualifiers
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                                                                                                                                                                                                         /note="Vector; pBluescript sk(-); Site_1: EcoRI;
XhoI"
                                                                                                                                                                                                                                   /tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
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/db_xref="taxon:9606"
/clone="NPCDBD10"
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Search completed: January 8, 2002, 15:13:30 Job time: 4806 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

REFERENCE AUTHORS

ORGANISM

Unknown. Unclassified.

TITLE

SUMMARIES

BASE COUNT ORIGIN

3258 a

organism="unknown" 2818 c 2717 g Location/Qualifiers

3140 t

FEATURES

JOURNAL source

target cells Patent: US 6200560-A 13 13-MAR-2001;

1 (bases 1 to 11933)
Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated virus vectors for expression of factor VIII by

RESULT 1 ARI38377 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE		11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	n T
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33 bp DNA m patent US 6200560. 14480722	ALIGNMENTS	AR138377 AR146887 AR146888 AR146888 AR034084 AR071336 AR071326 AR071326 AR07137 AR052730 I71409 IF1409 IF14	ID
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                                            1 cagetgegegetegeteaetgaggeegeeegggeaaageeegggegtegggee 60
                                                                                                                                                 GCTGTTGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATCAGACCAGT
                                                                                                                                                               gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840
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661 aacatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgag
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                                             ttcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc 660
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                              TTCAACACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTC
                                                                                       GATCTCGGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCA
                                                                                                                                               AGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGT
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                                                                                                      186 GATGTCGTGTACTGGCTCC---GCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGT
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291 CGGCAGGTAAGTGCCAGGGAATGTTTGTTCTTAAATACCATCGCTCCAGGGAATGTTTGT 350
             301 aggcaggtaagtgccgtgtgtgggttcccgcggggcctgggccttttacgggttatggccct 360
                                                  243 GCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTT-----TGCCGCCCCG 290
                                                                    241 aaagaagtatattagagogagtotttotgoacacagatcacctttocgggtgccgcccct 300
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                                                                                                                                                        ACTAGGGGTTCCTGCGGCCGCGCGTGGTGGCGCGGGGTAAA-----CTGGGAAAGT 185
                                                                                                                                                                                                                                                                                                                   859;
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Couto, L.B., Colosi, P.C. and Qian, X.
Adeno-associated virus vectors for expression
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Couto, L.B., Colosi, P.C. and Qian, X.
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Voorberg, J.J.
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                                                Hybrid proteins with modified activity Patent: US 6130203-A 1 10-OCT-2000;
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/trans1_table=11
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/protein_id="CAA00448.1"
/db_xref="GI:345062"
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VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVEPGGSHTYVWQVL
                     /translation="MQIELSTCFFLCLLRFCFSATRRYYLGAVELSWDYMQSDLGELP
                                                                                                     /organism="synthetic construct"
/db_xref="taxon:32630"
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246 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 486 caccagaagatactacctgggtgcagtggaactgtCatgggactatatgcaaagtgatct 545 426 catgcaaatagagctctccacctgcttctttctqtgcgctttttgcgattctgctttagtgc 485 66 CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 125 6 CATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTGCGATTCTGCTTTAGTGC 65 tggtgtatcetaetggaaagettetgagggagetgaatatgatgateagaeeagteaaag TGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGT tgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgt 785 cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT 245 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665 h 57.5%; Score 575; DB 6; Length 8241; Similarity 100.0%; Pred. No. 5.1e-164; 2625 a Conservative KWAEANREGEVEPELVAJASSAKTEPSKILDELAMONHSGTOLEKEEWKSQEKSPEKTA FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKGGRTERLCSQNPPVLKRHQRE ITRTTLGSDQEELDYDDTISVEMKKEDEPDIYDEDENGSPRSTOKTRHYFIAAVERLW DYGMSSSPHLLANRAGSGSVPOFKKVVFQEFTDGSFTQPLYRGEKTRHYFIAAVERLW EVEDNIMVTERNQASGSVPOFKKVVFQEFTDGSFTQPLYRGEKTRHYFIAAVERLW EVEDNIMVTERNQASRPSSFYSSIISYEEDQRGGAEPRKNYVKPNETYTYFWKVQHHM AFTKDEFDCKAMAYFSDYDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT IFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRTHAINGYLMPGTLYPGLVMAQDQR LQVDBÖKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ DSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY" YEDTITLEPSGETVEMMENPGLING
YEDISAYLLSKNNAIEPRSENSKHILGCHNSTENRKATIPEMDIEKTDEWFAHRTEN
PKIQNVSSSDLLMLRQSPTPHGLSLSDLQEAKYETFSDDSSPGAIDSNNSLSEMTHF
ROQLHHSGDMVETFESGLQERLEKLGTTAATELKKLDFKVSSTSNNLISTIPSDNLA
AGTDNTSSLGEPSMPVHYDSQLDTILFEKKSPLTESGEPLSLSEENNDSKLLESGLA
MSOESSWGKNVSSTESGRLFKGKRAHGPALLTKDNALFKVSISLLKTWRTSUNSATNR
KTHIDGESLLIENSPSVWQNILESDTEFKKTPLIHRRLMDKNATALRLNHMSNKTT
SSKUMEMVQQKKEGPIPPDAQNPDMSFFKMLFLESARWIQRTHGKNSLNSGQGPSPR OLVSLGPEKSVEGONFLSEKNKVVVGKGEFTKDVGLKEMVFPSSRNLELTNLDNLHEN NTHNOEKK I OEEI EKKETLI OENVVLPO I HT VTGTKNFMKNLFLLSTRONVEGSYDGA YAPVLODFRSLADSTNETKKHTAHFSKKGEEENLEGLGNOTKO I VEKYACTTRI SPNT SONVFYTORSKRALKOFRLPLEETELEKR I I DUDTSTOWSKNMKHLT PSTLTOJ DY NE KEKGA I TOSPLSDCLTRSHS I TOANRSPLP I AKVSSFPSI RPI YLTRVLFOONSSHLP AASYRKKDSCYOESSHE LOGAKKNNLSLA I LTLEMTGDOREVGSLGTSATNSVTYKKV ENTVLPKPDLFKT SGKVELLPKVHI YOKDLFFTETSNOSPGHLDLVEGSLLOCTEGA I NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEW TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMEWMGCDL VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAGIWR PEFOASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMV TDETFKTREAIOHESGILGPLLYGEVGDTLLIIFKNOASRPYNTYPHGITDVRPLYSR RLPKGVKHLKDFPILPGEIFKYKWTVTVEDGPTKSDPRCLTRYYSSFVNMERDLASGL IGPLLICYKESVDQRGNQIMSDKRNVILFSVFDENRSWYLTENIQRFLPNPAGVQLED VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY QHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFTQIRS KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTOTLHKFILLF AVEDECKSWIBETKNSLMODRDAASARAWPKMHTVNGYVNRSLPGLIGCHRKSVVWHV IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGOFLLFCHISSH 1759 c . Mismatches 1703 g 0; Indels 0; Gaps 365

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366 TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG

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Van Ooyen, A.J., Andreoli, P.M., Van Mourik, J.A. and Pannekoek, H. Method for the preparation of proteins with factor VIII activity by microbial host cells; expression vectors, host cells, antibodies Patent: EP 0253455-A 23 20-JAN-1988;
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                                                                             KWNEANRPGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTA
FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQRE
ITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
                                                                                                                                                                                                      AASYRKKDSGVQESSHFLQGAKKNNLSLAILTLENTGDQREVGSLGTSATNSVTYKKV
ENTVLPKPDLPKTSGKVELLPKVHIYQKDLFPTETSNGSPGHLDLVEGSLLQGTEGAI
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IGMGTTPEVHSIFLECHTFLYRNHROASLEISPITFLTAOTLLMDLGOFLLFCHISSH
OHDGMEAYVKVDSCPEEPQLRMKNDEAEDYDDDLTDSEMDVYRFDDDNSPSFJOIRS
VAKKHEKTWYHYIAAEBEDWDYAPLVLAPDDRSYKSOYLNUGPORIGRKYKKVFFMAY
TDETFKTREAIOHESGILGPLLYGEVGDTLLIIFKNOASRPYNIYPHGITDVRPLYSR
RLPKGYKHLKDFPILFGEIFKKKWTVTVVEDGFTKSDPRCLTRYYSSEVNMERDLASGL
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KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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Patent: JF
GENENTECH
                                                                                                                                                                                                                                       Complete cDNA encoding human factor VIII
               Danieru,J.K., Richiyaado,M.R., Goodon,A.B. and Uiriamu,A.U. MANUFACTURE OF FUNCTIONAL VIII FACTOR Patent: JP 1985243023-A 2 03-DEC-1985;
                                                                                                                                        Homo sapiens
                                                                                                                                                                          E00527.1 GI:2168806
JP 1985243023-A/2.
                                                                           Mammalia; Eutheria; Primates; 1 (bases 1 to 8831)
                                                                                                                  Eukaryota; Metazoa; Chordata;
                                                                                                                                                             Homo sapiens.
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DSTPPVWSLDPPLLTWYLIRIHPOSWVHGIALKMEVLGCEAQDLY"

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100.0%; Pred. No. 5.1e-164;
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PD 03-DEC---
PR 20-APR---
PR 20-APR---
PR 20-APR---
PI DANIERU
ARENU BIIHAA,
PI UIRIAMU
PC 612N5/0
PC C12N15/0
CC 12N15/0
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CC hypothe
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                                                                                                 TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG
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03-DEC-1985
19-APR-1985 JP 1985085295
20-APR-1984 US 84 6023
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Key Location/Qualifiers
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7266. .<8967
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1 (bases 1 to 8967)
Saenko,E.L. and Strickland,D.K.
Methods of reducing factor viii clearance and compositions therefor Patent: WO 0071714-A 1 30-NOV-2000;
The American National Red Cross (US)
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IGMGTTPEKTKSLINGDEDAASARAMPKMITVINGYVINSLIGGLIGGHKKSYVMHV
IGMGTTPEKTKSLINGDEDAASARAMPKMITVINGYVINSLIGGLIGGHKKSYVMHV
OHDGMEAYVKVUSCEBEPOLRMKINEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQIRS
VAKKHPKTWHY LAAEEDMDVAPLUAAPDDRSYKSQYLINIGPORIGRXYKKVRFMAY
RLPKGYKHLKOFPILPGEIFKYKMTVTVEDGPTKLIIFKNQASRPYNIYPHOITDVRSPLYSR
RLPKGYKHLKOFPILPGEIFKYKMTVTVEDGPTKLIIFKNQASRPYNIYPHOITDVRSPLYSR
RLPKGYKHLKOFPILPGEIFKYKMTVTVEDGPTKLIIFKNQASRPYNIYPHOITDVRSPLYSR
IGPLLICYKESVODGROQIMSDKRIVILFSVFDENRSWYLTENIQRFLPNPAGVQLED
PEPQASNIMHSINGYVFDSLGLVCHEWAYWYILSIGAQTDPLSVEPSGYTPKKMW
SYEDISAYLLSKNAAIFERSFSQNSRHRSTRQKOFNATTI PENDIEKTDPWFAHRTPN
SYEDISAYLLSKNAAIFERSFSQNSRHRSTRQKOFNATTI PENDIEKTDPWFAHRTPN
SYEDISAYLLSKNAAIFERSFSQNSRHRSTRQKOFNATTI PENDIEKTDPWFAHRTPN
RQLHHSGIMVFTPESGLOLRLMEKLGTTAATELKKLDFKVSSTSNNLISTIPSDNLS
SYENTSSLGPPSMPVHYDSQLDTTLFGKKSSPLFLSSGESNIKTTSDNLS
SYENTHF
RGTUNTSSLGPPSMPVHYDSQLDTTLFGKKSSPLFSSDESSRAIFRTNKTSNNSATIN
SSKIMMEMVQOKKEGPIPPDAQNIESDTEFKVTPLIHDRMLMDKNATALRLNIMSNKTT
SSKIMMEMVQOKKEGPIPPDAQNIESDTEFKVTPLHDRMLMDKNATALRLNIMSNKTT
SKRMMEMVQOKKEGPIPPDAQNIESTHEKTHVDTSTROWSRINFTINIDNLHEN
VAPVLODERSLUSSTNRTKHTAHFSKKGEENNLEGLGNGTMGVTKKVESVAGCTTRISPNT
KERGATTQSPLSDCLTRSHSIPPLAHFSKKGEENNLEGLGNGTKOTKOTTSTURTKKY
SQOMFVTGRSKRALKOFRLPLEETELEKRIIVDDTSTOWSKINKHLIPSTLTQIDVK
SQOMFVTGRSKRALKOFRLPLEETELEKRIIVDDTSTOWSKINKHLIPSTLTQIDVK
KEKGATTQSPLSDCLTRSHSIPPLAARSPLPIAKVSSPSIRPIYLTRVLFQDNSSHLP
AASYRKDSGVOESSHFOGAAKNINJSLAITTLEMTGDDREVGSLGTSATNSVTYKKV
KWNEANRPGKVPFIRVATESSAKTPSKILDELFFTSNGSPGHLDLVEGSLLQGTSGATNSVTYKKV
KWNEANRPGKVPFIRVATESSAKTPSKILDDIAMNNAMNHVGTOTOTEKFRAKKGTEKSORKFTA
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                                                                                                                                                                                                                                FKKKDTILSLNACESNHAIAAINEGONKPEIEVTWAKOGRTERLCSONPPVLKRHORE
ITRTTLOSDOEEIDYDDTISVEMKKEDFDIYDEDENOSPRSFOKKTRHYFIAAVERLW
DYGMSSSPHVLRNRAOSGSVPOFKKVVPOEFTDGSFTOPLYRGELNEHLGLLGPYIRA
TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
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                                                              VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY
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/db_xref="GI:12226921"
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/db_xref="taxon:9606"
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649 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 683
                 966 tgtggacctggtaaaagacttgaattcaggcctca 1000
                                                           589 GAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCA
                                                                            906 gaaagaaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca
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                                                                                                                                             tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
                                                                                                                                                                                                                                                         TGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCCATCCTGTCAGGTCTTCATGCTGT 468
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167. . 7162
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DEFINITION
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                                                                          AUTHORS
TITLE
                                                             JOURNAL
                                                                                                                                 ORGANISM
                                source
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                 1 (bases 1 to 8967)

Bodner, M., De Polo, N.J., Chang, S., Hsu, D.Chi-Tang and Respess, J.G. Retroviral delivery of full length factor VIII

Patent: US 5681746-A 1 28-0CT-1997;
Location/Qualifiers
1. 8967
                                                                                                                              Unknown.
                                                                                                                  Unclassified.
                                                                                                                                                                                      Sequence 1 from patent US 5681746. 171409
                                                                                                                                               Unknown.
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/organism="unknown"
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                                                                                                                              Wood, W.I., Capon, D.J., Simonsen, C.C., Eaton, D.L., Gitschier, J., Keyt, B., Seeburg, P.H., Smith, D.H., Hollingshead, P., Wion, K.L., Delwart, E., Tuddenham, E.G.D., Vehar, G.A. and Lawn, R.M. Expression of active human factor VIII from recombinant DNA clones Nature 312 (5992), 330-337 (1984)
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                               Human mRNA for factor VIII.
                                                                                                                                                                                                                                                                                                                            HSFVIIIR
                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8967)
                                                                                                                                                                                                                                                                      factor VIII; signal peptide.
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                                                                                                          Data
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                                                                                                          kindly reviewed (20-MAR-1986) by W. Wood
             /note="5' untranslated region" 110. .166
/product="signal peptide (aa -19 to -1)"
                                                  /db_xref="taxon:9606"
                                                                    /organism="Homo sapiens"
                                                                                           Location/Qualifiers
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546 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa
                                                                                                  169 CACCAGAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 228
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
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IGMGTTPEVHSIFLEGHTF LVRNHROASLEISPITGLTAQTILMOLOGFLIFGHISSH
IGMGTTPEVHSIFLEGHTF LVRNHROASLEISPITGLTAQTILMOLOGFLIFGHISSH
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RLDKGYKHLKDEP ILOGEIFKYWTYUTUDGPTKSDPFCLITRY YSSFVNHEEDLASGL
PSTOLICH YSSTOLICH INGYVEDDEN ILOGEIFKYWTYUTUDGPTKSDPFALLKYSSFVNHETDWFAHRTPM
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/translation="MQIELSTCFFLCLLRECFSATRRYYLGAVELSWDYMOSDLGELP
VDAREPPRVPKSEPFNTSVVYKKTLEVEFTDHLENIAKPRPPWMGLLGPTIQAEVYDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110. .7165
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/db_xref="GI:31499"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVFDEGKSWHSETKNSLMODRDAASARAWPKMHTVNGYVNRSLPGLIGCHRKSVYWHV
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KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITRTTLQSDQEELDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
DYGMSSSPHULRURAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELUEHLGLLGPYIRA
EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
APTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="3/ nr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="mature factor VIII (aa 1-2332)" 7163. .8967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGOYGQMAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYIMDTLPGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETVEMLPSKAGIWR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ
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                                                                                                                                                                                                                                                                                                                                                                                                                              57.5%; Score 575; DB 9; L
100.0%; Pred. No. 5.2e-164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            906 gaaaggaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409 TGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGT 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            349 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 caccicagitegigitacaaaaagacitetgitigitagaaticaeggaiteaccititicaacai 665
[2] sites; mutations causing hemophilia.

Draft entry and clean copy sequence for [1] kindly provided by M.A.Truett, 26-FBB-1986.

The mutation at position 1042 results in a change of Glu to Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99agaaagaagatgataaagtottocotggtggaagcoatacatatgtotggcaggtoot 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG
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                                                                                                                                88197150
                                                                                                                                                                    DeRosa,V. and Marchetti,G.
A HindIII RFLP and a gene lesion in the coagulation factor VIII
                                                                                                                                                                                                            s (sites)
Bernardi,F., Legnani,C., volinia,S., Patracchini,P., Rodorigo,G.,
                                                                                                                                                                                                                                                                             Moderately severe hemophilia A resulting from Glu----Gly substitution in exon 7 of the factor VIII gene Am. J. Hum. Genet. 42 (6), 867-871 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGTGAGCTGCCTGTGGAGGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAA 288
                                                                                                                                                                                                                                                                                                                                                            Youssoufian, H., Wong, C., Aronis, S., Platokoukis, H., Kazazian, H.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Characterization of the polypeptide composition of human factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Truett, M.A., Blacher, R.W., Burke, R.L., Caput, D., Chu, C., Dina, D., Hartog, K., Kuo, C.H., Masiarz, F.R., Merryweather, J.P., Najarian, R. Pachl, C., Potter, S.J., Puma, J., Quiroga, M., Rall, L.B., Randolph, A. Urdea, M.S., Valenzuela, P., Dahl, H.-H.M., Favalaro, J., Hansen, J., Nordfang, O. and Ezban, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIII:C and the nucleotide sequence and expression of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 9029)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coagulation factor VIII:C.
Human kidney, cDNA to mRNA, clones pF8[100,102]; and cell line
GM1416 DNA, clone pF8-4.3.
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                                                                                                                                                                                                                                                                                                                                                       and Antonarakis, S.E.
                                                                                                                                      Genet. 78 (4), 359-362 (1988)
                                                                                              sites; mutation causing hemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                        (5), 333-349 (1985)
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variation

6853

/gene="F8C"

/gene="F8C"

/note="a in wt; g in hemophiliac [2]"

/note="g in wt; a in hemophiliac [2]"

/gene="F8C"

variation

variation

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FEATURES
                                                                                                   mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARKIPKTWYHY LAAEEEBMUZAELY DUDLITDSEMDVVRFDDDNSPSFIQIRS
VAKKIPKTWYHY LAAEEEBMUZAELV GEVGYTLLI EKNQASRPYNITYHOGTOTRYKYKFWAPAY
TDETFKTRAIQHESGILGPLLYGEVGDTLLI EKNQASRPYNITYHOGTOTRYBLYGY
RLPKOYKHLKDFPLLPGELFK YKRTVTVEDGPTKSDPRCLTRYSSFVNMEDLASGL
IGPLLICYKES VODGROLIMS DKRINVILFSVEDENRSWITENIQFFLENBAGVQLED
YEDTLTLFPSGETVFMSMENPGLIWILGCHNSDFRINGMTALLKVSSCDKNTGDYYED
YEDTLTLFPSGETVFMSMENPGLIWILGCHNSDFRINGMTALLKVSSCDKNTGDYYED
YEDTLTLFPSGETVFMSMENPGLIWILGCHNSDFRINGMTALLKVSSCDKNTGDYYED
YEDTLTLFPSGETVFMSMENPGLIWILGCHNSDFRINGMTALLKVSSCDKNTGDYYED
YEDTLTLFPSGETVFMSMENPGLIWILGCHNSDFRINGMTALLKVSSCDKNTGDYYED
YEDTLTLFPSGETVFMSMENPGLIWILGCHNSDFRINGFTLDSNISLSEMTHF
SYEDIESAYLLKSKINALIERRSFSONSRIPSTROKOFNATTI PENDIEKTDPWFAHRTPM
YEDTLTLFPSSGETVFMSMENPGLIWILGCHNSDFRINGFTSDBPSGAILDSNISLSEMTHF
ROTHHSSULGPENSFSONSHIPSTROKOFNATELKKLDFKVSSTSUNLISTISDNISLSEMTHF
ROTHHSSLIGPESMPHYDSQLDTTLFGKKSSPLTESGGPLSLSEENNDSKLLESGLIA
NSQESSWGKNVSSTESGRLFKGKRAHGPALLTTNDNALFKVSISLIKTINKTSNISATIN
SSKIMENVOOKKEGP IPPDAQNPDMSFFKMLFLLPSARWIDFRHGKNSLNSCOGPSPR
QLVSLGPEKSVEGQNFLSEKNKVVVGKGEFTKNOFLKEMVPPSSRILLFTNLDNLHEN
VAPVLODERSLOOLTISMSSYMONILESDTEFKKVTPLILDRALMDKNATALRLHINSUKTT
SKNMENPOOKKEGP IPPDAQNPDMSFFKMLFLFLSARWIDFRHGKNSLNSCOGPSPR
QLVSLGPEKSVEGUNFLSEKNKVVVGKGEFTKNOFLKMVLFLLSTROKNESVOGA
SQONFVTORSKRALKOFLPLEETELEKRITVDDTSTOMSKNMKHLFLFSTLTOIDVKR
VAPVLODERSLNOSCHIEBTLESTELEKRITVDDTSTOMSKNMKHLFLFSTLTOIDVKN
AASYKKALOSCHUSSHLP
EKTVLRKOSCHUSDDTISWSHLP
EKTVLRKPDLLRTGSKYLLCHANDSHARGOOKSPEIDTSNGSPGLLOGTEGAI
FKKNDTILSLANACESHAIAAANERGOOKPEITSNGSPGHLDLVEGSLLOGTEGAI
FKKNDTILSLANACESHAIAAAANERGOOKPEITYDEDENSPROKAKNORTHAAVERLW
DYGMSSSPHVLRNAOSGSVPOOKKVVFOOFTORSFTONINGSFTONINGSTRALAGVERLW
DYGMSSSPHVLRNAOSGSVPOOKKVVFOOFTORSFTONINGSFTONINGSTRALAGVERLW
DYGMSSSPHVLRNAOSGSVPOOKKVVFOOFTORSFTONINGSFTONINGSTRALAGVERLALLT
                                                                                                                                                                                                                                                                                                                                                      APTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
IFDETKSWYETENNERNCRAPCNIQMEDPTFKENYRFHAINGY IMDTLPGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEEYKMALYNLYPGVFETYEMLPSKAGIWR
                                                                                                            DSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY"
                                                                                                                                                NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPOVNNPKEW
LQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ
                                                                                                                                                                                                                                 TYRGNSTGTLMVEFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
                                                                                                                                                                                                                                                                         VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIMYSLDGKKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYGMSSSPHŸLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHLGLLGPYTRA
EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
note="coagulation factor VIII:C"
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IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDARFPPRVPKSFPENTSVVYKKTLEVEFTDHLFNIAKPRPPWMGLLGPTIQAEVYDT
VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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/db_xref="GI:182818"
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172. .7227
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                                                         1 (bases 1 to 7272)
Sarver, N. and Drohan, W.
Fractor VIII-C analogs
Patent: ED 0265778-A1 3 04-MAY-1988;
Location/Qualifiers
1. 7272
                                                                                                                                                       Sequence 3 from Patent EP 0265778
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1591 c 1533 g
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100.0%; Pred. No. 5.2e-164;
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541 GTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 574
         967 gtggacctggtaaaagacttgaattcaggcctca 1000
                                  907 aaagagaattygtccaattggcctctgacccactgtgccttacctactcattatcttctcat 966
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Search completed: January 8, 2002, 17:15:54 Job time: 12045 sec

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Listing first 45 summaries
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1 2 3 3 5 5 6 6 7 7 10	Result No.	
1000 1000 725.2 725.2 725.2 617.4 577.4 575.8 575.8	Score	
100.0 11933 21 AAD00121 100.0 11933 22 AAD08612 72.5 4999 21 AAD08613 72.5 4999 22 AAD08613 61.7 7944 22 AAF84647 61.7 5035 18 AAF69811 57.7 12445 21 AAA49232 57.6 11846 20 AAX822261 57.6 11846 20 AAX822261 57.6 12022 20 AAX822260 57.5 4832 19 AAV19581	Query Match Length DB ID	di
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119 119 119 119 119 119 119 119 119 119	19
AANS1439 AANS1439 AANS1096 AANS10054 AANS20054 AANS20054 AANS20054 AANS20580 AANS1544 AANS20580 AANS1547 AANS205810 AANS21652 AANS21652 AANS21652 AANS21654 AANS21656 AANS2166615 AANS2166615 AANS2166615 AANS2166615 AANS2166689 AANS2258 AANS2258 AANS2333 AANS23689 AANS2337 AANS2364 AANS2338 AANS2337 AANS24664 AANS23339	AAV15338
Factor VIII cDNA 1 CDNA sequence enco Factor-VIII full-1 Human factor VIII Factor VIII:C codi Human factor VIII:C codi Human factor VIII Factor VIIII Factor VIIII Human factor VIII Mono sapiens facto B-domain deleted F Sequence encoding cDNA encoding huma Beta-domain delete DNA sequence encod Modified factor VI Modified factor VI Human factor VI Human factor VIII Human factor VIIII Human factor VIIII Human factor VIII Human factor VIII Human factor VIIII Human factor VIII Human factor VIIII Human factor VIIII Human factor VIIII Human factor VIII Human factor VIIII Human factor VIII Human factor VIIII Human factor VIIII Human factor VIII Human factor VIIII Human factor VIII Human factor VIIII H	Human Factor VIII Factor-VIII cDNA.

ALIGNMENTS

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AAD00121
AAD00121 standard; DNA; 11933 BP.
                                                                                                   AAD00121;
                                                                                           31-JUL-2000 (first entry)
                                                                                   Recombinant adeno associated vector construct, pAAV-F8-1.
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RESULT

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Recombinant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor VIII; htvIII; HNF-3 albumin promoter; human elongation factor-lalpha; EFlalpha; human growth hormone; hGH; inverted terminal repeat; ITR; haemophilia; gene therapy; ds.

Adeno associated virus.

WO200023116-A1

27-APR-2000.

19-OCT-1999; 99WO-US24495.

20-OCT-1998; 24-MAR-1999; 30-JUL-1999; 98US-0104994. 99US-0125974. 99US-0364862

(AVIG-) AVIGEN INC.

Couto LB, Colosi PC;

WPI; 2000-339536/29

New recombinant adenovirus-associated vector, useful for gene therapy

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Query Match
Best Local Similarity
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601 ttcaacacctcagtcgtgt<mark>g</mark>caaaaagactctgtttgtagaattcacggatcaccttttc 660
                                          541 gatctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcca
                                                              541 gatctoggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcca 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hrvIII coding region comprises the heavy chain gene segment with the and 5 amino acids from the N-terminus of the B domain. The light chain segment comprises the c-terminal 85 amino acids of B domain and the A3 domains segment comprises the C-terminal 85 amino acids of B domain and the A3 into the same plasmid seperated by 42 nucleotides coding for 14 residues control sequences, that directs the transcription and translation of the B domain, that is deleted. This plasmid is operably linked to factor VIII gene. The adeno-associated viral vectors are used for gene therappy, because of their broad host range, safety profile and duration of the thorapy, because of their broad host range, safety profile and duration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF-3 albumin promoter, the first intron (-573 to +985) of human elongation factor-lalpha (EF1alpha) gene, human Factor VIII coding sequence (hFVIII) and polyadenylation signal from human growth hormone (hGH). This sequence is inserted between the AAV inverted terminal repeat (ITR) regions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 tttggtcgcccggcctcagtgagcgagcgagcgcgcagagagggagtggccaactccatc 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 cagctgcgcgctcgctcgctcactgaggccgcccgggcaaagcccggggcgtcggggacc 60
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                                                                                                                                                                                                                                                                                                                                                                                        aggcaggtaagtgccgtgtgtggttcccgcggggcctggcctctttacgggttatggccct
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δÃ Вb γQ В δõ Дb Ş DЪ δã В δõ В Ş 밁 ρy DЪ δÃ Ъ δÃ В

The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprisis a nucleotide sequence encoding the light chain of factor VIII and a second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector i

comprising

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AAD08612
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                                                                                        Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood coagulation factor \rm VIII
                                                                       Claim 18; Fig 5; 90pp; English
                                                                                                                                                                       Couto LB, Colosi PC, Qian X;
                                                                                                                                                  WPI; 2001-417955/44.
                                                                                                                                                                                                (AVIG-) AVIGEN INC
                                                                                                                                                                                                                       22-DEC-1999;
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                                                                                                                                                                                                                                                                                                            Chimeric - Oryctolagus cuniculus
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                                                                                                                                                                                                                                                                                                                                                Chimeric - Adeno associated virus
                                                                                                                                                                                                                                                                                                                                                                             blood clotting disorder; gene therapy; haemophilia A; human;
                                                                                                                                                                                                                                                                                                                                                                                       Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                             Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
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gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840
                  gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840
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              The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct pVm4.1cp8deltaB. This expression vector comprises the CC promoter, first intron (-573 to +995) of human elongation factor-lalpha CC promoter, first intron (-573 to +995) of human elongation factor-lalpha CC promoter first intron (-573 to +995) of human elongation factor-lalpha CC polyadenylation signal from human growth hormone (hGH). This sequence is CC promoter that AV inverted terminal repeat (ITR) regions. The CC promoter for the AAV inverted terminal repeat (ITR) regions. The CC promoter for the N-terminus of the Bomain. The light chain CC and 5 amino acids from the N-terminus of the Bomain. The light chain segment comprises the C-terminal 85 amino acids of B domain and the A3. CC segment comprises the C-terminal 85 amino acids of B domain and the A3. CC control sequences, that directs the transcription and translation of the CC control sequences, that directs the transcription and translation of the Factor VIII gene. The adeno-associated viral vectors are used for gene CC therapeutic levels of factor VIII in vivo. The rAAV are used for gene CC therapy, because of their broad host range, safety profile and duration CC of expression in the infected hosts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; ds.
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24-MAR-1999;
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961 tctcatgtggacctggtaaaagacttgaattcaggcctca 1000
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                                             gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt
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                                                                                                                                                                                                9Ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840
                                                                                                                                                                                                                                                               9tttatgatacagtggtcattdcacttaagaacatggcttcccatcctgtcagtcttcat 780
                                                                                                                                                                                                                                                                                                                                                                                                                                            gatctcggtgagctgcctgtggacgcabgatttcctcctagagtgccaaaatcttttcca
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                                                                                                                                                                                                                                                                                                                                                                              ttcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc
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Pred. No. le-198;
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Qy дg Qy DЬ

121 actaggggttcctgcggccgcccagggaatgtttgttcttaaataccatccagggaatgt 180

73 tttggtcgcccggcctcagtgagcgagcgagcgcgcagagagggagtggccaactccatc

tttggtcgcccggcctcagtgagcgagcgagcgcgcagagagggagtggccaactccatc 120 cagctgcgcgctcgctcactgaggccgcccgggcaaagcccgggcgtcgggcgacc 72 Ωy

1 cagctgcgcgctcgctcgctcactgaggccgcccgggcaaagcccgggcgtcgggccc

Matches 859; Query Match

Local

Similarity

72.5**%**; 85.9**%**;

Score 725.2; DB Pred. No. 1e-198;

DB 22;

Length 4999;

Conservative

0; Mismatches 118; Indels

23; Gaps

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Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other;

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В
950 tctcatgtggacctggtaaaagacttgaattcaggcctca 989
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CC The present invention relates to a method for treating a subject CC suffering from a blood clotting disorder. The method comprises CC administering a recombinant adeno-associated virion (rAAV) comprising CC anuclectide sequence encoding the light chain of factor VIII and a CS sequence encoding the heavy chain of factor VIII. The rAAV vector is CC useful in gene therapy for treating haemophilia A in mammals, in CC particular humans. The rAAV vector provides high level and long term CC expression of biologically active clotting factor VIII in vivo. CC The present sequence is pVm4.1cF8-B vector without the plasmid Backbone. It comprises human elongation factor I (EFI) promoter, CC and AAV inverted terminal repeats (ITRs) at the ends. The vector CC and AAV inverted terminal repeats (ITRs) at the ends. The vector CC encodes both the light and heavy chains of human factor VIII coding sequence, poly A signal CC encodes both the light and heavy chains of human factor VIII
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                                                                                                                                                                                                                                                                                                                                                                      Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood coagulation factor {\tt VIII}
                                                                                                                                                                                                                                                                                                                                      Claim 19; Fig 6; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-417955/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Homo sapiens
Chimeric - Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AVIG-) AVIGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-2000; 2000WO-US34925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          blood clotting disorder; gene therapy; haemophilia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human factor VIII expressing rAAV vector pVm4.1cF8-B partial sequence
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133 actaggggttcctgcggcgcacgcgtggtggcgcgggggtaaa-----ctgggaaagt 185

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Synthetic

actaggggttcctor

181 ttgttcttaaataccatccagggaatgtttgttcttaaataccatctacagttattggtt 240

gatgtcgtgtactggctcc---gcctttttcccgagggtgggggagaaccgtatataagt 242

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tccaccatgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgcttt 480 tocaccatgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgctt 469

cggcaggtaagtgccagggaatgtttgttcttaaalaccatcgctccagggaatgtttgt 350 aggcaggtaagtgccgtgtgtggttcccgcggggcctcttttacgggttatggccct 360

B

351

QΥ В Qy

481 agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 540

agtgocaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 529

541 gatotoggtgagotgcotgtggacgcaagatttcotcotagagtgccaaaatcttttcca 600

gatotoggtgagotgootgtggaogcaagatttootootagagtgooaaaatottittooa 589

601 ttcaacacotcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc

ticaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttc 649

661 aacatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgag 720

gtttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcat 769

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781 gctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagt 840

770 gctgttggtgtatqptactggaaagcttctgagggagctgaatatgatgatcagaccagt 829

961 tctcatgtggacctggtaaaagacttgaattcaggcctca 1000

totoatgtggacotggtaaqagacttgaattcaggcotca 989

890 gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt

gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt 960

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector. The vector comprises a heterologous nucleotide sequence encoding B-domain deleted factor VIII operably linked with at least one encoding B-domain deleted factor VIII operably linked with at least one encoding B-domain deleted factor. The method results in the production enhancer and at least one promoter. The method results in the production of high titer raAv vector stocks carrying the B-domain deleted factor VIII transgenes and expression cassettes, which generate adequate titers virus for in vivo administration. The recombinant vectors are useful of virus for in vivo administration. The recombinant vectors are useful for treating haemophilia A, where the liver expresses the encoded B-domain deleted factor VIII, which is secreted into the blood. They are also useful for the treatment of other coagulation disorders. The present sequence encodes a B-domain deleted factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant adeno-associated virus vector, useful for treating haemophilia A, comprises heterologous nucleotide sequence encoding B-domain deleted human factor VIII operably linked with liver-preferred expression control element .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Walsh CE, Chao H, Burstein H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 64; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes a recombinant adeno-associated virus (rAAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7944 BP; 2142 A; 1902 C; 1909 G; 1991 T; 0 other;
                       124 aggggttcctgcggccgcccagggaatgtttgttcttaaataccatccagggaatgtttg 183
135 aggggttcct----
                                                                                                                                                                                                                                                                                                                    Local Similarity
les 783; Conserva
                                                                                                15 ctgcgcgctcgctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccgggcttt 74
                                                                                                                                                                                                                                     4 ctgcgcgctcgctcgctcactgaggccgccgggcaaagcccggggcgtcggggcgaccttt 63
                                                                                                                                                                                                                                                                                                                                Conservative
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/note= "inverted terminal repeat"
150..278
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/note= "TK polyA sequence"
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/note= "human B-domain deleted factor VIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4916..5084
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                                                                                                                                                                                                                                                                                                                                                                61.7%;
78.5%;
           ----cagatetetttetaagtaaacagtacatgaacettt 180
                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                Score 617.4; DB 22; Length 7944; pred. No. 1.4e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lynch CM,
                                                                                                                                                                                                                                                                                                                                            Mismatches 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stepan AM,
                                                                                                                                                                                                                                                                                                                                                          Indels 18; Gaps
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XGXAX
XXXXX
                                                                                                  AAF84647 standard; DNA; 7944 BP
                                      Plasmid DLZ6 encoding human :B-domain deleted factor VIII.
                   Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;
                                                             29-JUN-2001
          coagulation disorder; ss.
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                                                              (first entry)
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AAT69811
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Homo sapiens.
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                   haemophilia; gene therapy; ss.
                                      Factor VIII-db695-HCII; heparin cofactor II; blood coagulation;
                                                                                  Factor VIII-dB695-HCII DNA.
                                                                                                          10-AUG-1997 (first entry)
                                                                                                                                                          AAT69811;
                                                                                                                                                                         AAT69811 standard; DNA; 5035 BP.
                     lood clotting; procoagulant; anticoagulant; antithrombotic;
                                                                                                                                                                                                                                                               964 catgtggacctggtadaagacttgaattcaggcctca 1000
                                                                                                                                                                                                                                                                                                957 catgtggacctggtaaaagacttgaattcaggcctca 993
                                                                                                                                                                                                                                                                                                                                                          777 gttggtgtatoctactggaaagcttotgagggagotgaatatgatgatcagaccagtcaa 836
                                                                                                                                                                                                                                                                                                                                                                                                                                   784 gttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaa 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             724 tatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatgct 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717 tatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatgct 776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        657 atcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggtt 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  604 aacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaac 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544 ctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattc 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 gtgccttgaattactgacattgacatccactttttctttttctccacaggtatcgattcc 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 aagcaaaaagceteteeaceeaggeetggaatgttteeaceeaatgtegageagtgtggt 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 cagginangigeogigigigigitecegegggeetgggeetetttaegggitaliggeeetige 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 ttettaaataceateeagggaatgittgitettaaataceatetaeagitattggitaaa 243
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                        total liver cDNA, fusion to sequences encoding Factor VIII aa706-711 and aa737-743, and incorporation of the construct into using gene therapy techniques, has increased procoagulant activit othe HCII acidic region, and can be used to treat blood coagulation disorders such as haemophilia A.
Sequence 5035 BP; 1484 A; 1127 C; 1110 G; 1314 T; 0 other;
                                                                                                             (Pactor VIII de1868-1562) B-domain are replaced by amino acids 51-80 from the acidic region (and potential thrombin-binding site) of human heparin cofactor II (HCII). It was obtd. by PCR amplification (see also AAT65912-13) of the HCII acidic region from
                                                                                                                                                                      A DNA molecule (AAT59811) codes for Factor VIII-dB695-HCII (AAW18670), a hybrid protein in which amino acids 712-736 of Factor-dB695
                                                                                                                                                                                                                                Claim 16; Page 52-60; 96pp; English.
                                                                                                                                                                                                                                                   Hybrid Factor VIII with modified activity, comprises region from donor anticoagulant or antithrombotic protein - useful for treatment of coagulation disorders
                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW18670
                                                                                                                                                                                                                                                                                                                                                                            Voorberg JJ;
                                                                                                                                                                                                                                                                                                                                                                                                        (IMMO ) IMMUNO AG
                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-EP04977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= heparin cofactor II region (aa5]-8])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Product= Factor VIII-dB695-HCII
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35..5020
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330 titatgatacagiggicattacacttaagaacatggcttcccatcctgtcagicttcatg
             722 tttatgatacagtggfcattacacttaagaacatggcttcccatcctgtcagtcttcatg 781
                                                                          662 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg 721
                                                         270 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg
                                                                                                                                     602 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 661
                                                                                                                      210 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 269
                                                                                                                                                                                                    542 atotoggtgagotgcotgtggacgcaagatttoctoctagagtgccaaaatcttttccat 601
                                                                                                                                                                                    150 atctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccat
                                                                                                                                                                                                                                                                 482 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 541
                                                                                                                                                                                                                                                                                                                             422 ccaccatgcaaatagagctotoccacctgcttctttctgtgccttttgcgattctgcttta 481
                                                                                                                                                                                                                                                90 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 149
                                                                                                                                                                                                                                                                                                            30 ccaccatggadatagagctctccacctgcttctttctgtgccttttgcgattctgcttta 89
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 57.7%; Score 577.4;
99.8%; Pred. No. 3.5

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                         DB 18; Length 5035;
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osteopathic; antisickling; immunostimulant; gene therapy; collage; endothelial cell; peripheral blood; buffy coat cell; VEGF; PCR primer; vascular endothelial growth factor; bovine brain extract; haemophilia; ractor VIII; human; transgene; adenosine deaminase deficiency; ss; sickle cell anaemia; thalassemia; diabetes; alpha-antirypsin deficiency; alzheimer's disease; brain disease; heart disease; immune system defect; alzheimer's disease; brain disease; heart disease; immune system defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA49232 standard; DNA; 12445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vector HSQReNeo for transforming endothelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2000 (first entry) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemostatic; antianemic; antidiabetic; nootropic; neuroprotective; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     570 ctcatgtggacctggtaaaagacttgaattcaggcctca 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     962
                                                                                                                                                                              Expanding population of endothelial cells useful to biocompatibilize implantable medical devices comprises contacting buffy coat cells with collagen I coated surface in culture medium comprising vascular
                                                                                                                                                                                                                                                                                                                                                                                               24-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                           24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone
           The invention relates to a method for expanding the population of endothelial cells (EC) obtained from peripheral blood, by culturing, endothelial cells obtained from peripheral mammalian blood in the presence of a culture medium from peripheral mammalian blood in the presence of a culture medium containing vascular endothelial growth factor (VEGF) and free of bovine brain extract. EC are useful for treating hemophilia by introducing it into the blood stream of a mammal, so that an effective amount of
                                                                                                                                                                                                                                     WPI; 2000-412303/35....
                                                                                                                                                                                                                                                                                                                                                  (MINU ) UNIV MINNESOTA.
(UYEM-) UNIV EMORY.
                                                                                                                                    Claim 19; Fig 4; 53pp; English.
                                                                                                                                                                     endothelial growth factor
                                                                                                                                                                                                                                                                                                        (LOLL/) LOLLAR J S.
Factor VIII protein is secreted in the blood stream of the mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fracture; osteoporosis.
                                                                                                                                                                                                                                                                                                                                   HEBBEL R P.
                                                                                                                                                                                                                                                                       Lin Y, Lollar JS,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the vector HSQReNeo where the human factor VIII gene into which an enhanced green fluorescent protein coding sequence (HSQ) has been inserted, is subcloned. Transgenic EC transduced in vitro are useful for improving prosthetic implants EC is also useful for diagnosing clotting disorders where indication or disease is associated with a reduction in the activity of an enzyme. EC is also associated with a reduction in the activity of diseases including useful in gene therapy for treating the variety of diseases including adenosine deaminase deficiency, sickle cell anemia, thalassemia, adenosine deaminase deficiency, sickle cell anemia, thalassemia, such as Alzheimer's disease, heart diseases, defects in immune system, such as Alzheimer's disease, heart diseases, defects in immune system, for repairing bone fractures and to treat or prevent osteoporosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12445 BP; 3255 A; 2989 C; 2951 G; 3250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                         1003 acatcyctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 ccaccatgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgcttta 481
1303 ctcatgtggacctggtaaaagacttgaattcaggcctca 1341
                                                                           1243 teetgaaagagaatggteeaatggeetetgaeeeactgtgeettaeetaeteatatettt 1302
                                                                                                                                                      1123 ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtc 1182
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                  962 otcatgtggacctggtaaaagacttgaattcaggcctca 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg
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                                                                                                                                                                                                                                                     ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtc 841
                                                                                                tcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatcttt
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Pred. No. 5.8e-156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                1062
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AAX82259
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AAX82259 standard; cDNA; 9164 BP

18-AUG-1999 (first entry)

Beta-domain deleted Factor VIII protein encoding gene (uncorrected).

XW XXX DE XXX splicing pattern; RNA processing; gene regulation; beta-domain; Factor VIII protein; gene modification; gene therapy; clinical disorder;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC The invention describes novel genes and vectors exhibiting increased CC expression and novel splicing patterns. It provides a gene encoding a CC Factor VIII protein, that comprises one or more consensus or near CC consensus splice sites which have been corrected to increase expression. CC the expression of a gene, especially a Factor VIII gene. Genes containing CC levels and tissue-specific expression. The methods are used for CC introns, optimization and correction of consensus splice sites, addition of CC introns, optimization of 5' and 3' untranslated regions have optimized expression CC introns, optimization of 5' and 3' untranslated regions and increase in CC to treat a clinical disorder, to study RNA processing and/or gene CC regulation. The present sequence represents an uncorrected version of CC explaining deleted factor VIII protein encoding gene sequence (construct CC deleted factor VIII protein by correcting the consensus splice sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
1301 tttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatg 1360
                                                                   1241 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg 1300
                                                                                                                                        1181 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggttcaccttttca
                                                                                                                                                                                                                1121 atctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccat 1180
                                                                                                                                                                                                                                                                                   1061 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 1120
                                                                                                                                                                                                                                                                                                                                                         1001 ccaccatggaaatagagctctccacctgcttctttctgtgcctttttgcgattctgcttta 1060
                722 tttatgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatg
                                                                                      662 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg 721
                                                                                                                                                         602 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 661
                                                                                                                                                                                                                                                                                                      482 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 541
                                                                                                                                                                                                                                                                                                                                                                         422 ccaccatgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgcttta 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9164 BP; 2451 A; 2170 C; 2081 G; 2462 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genes and vectors exhibiting increased expression and novel splicing patterns, useful for expression of, e.g. beta-domain deleted factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1998;
05-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 57.6%; Local Similarity 99.7%;
                                                                                                                                                                                                                                  atctcggtgagctgcctgtggacgcaagatttccttcctagagtgccaaaatcttttccat 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 575.8; DB 20; Length 9164; Pred. No. 1.5e-155;
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                                                                 The invention describes novel genes and vectors exhibiting increased expression and novel splicing patterns. It provides a gene encoding a factor VIII protein, that comprises one or more consensus or near consensus splice sites which have been corrected to increase expression. The method, DNA sequences and expression vectors can be used to increase modified 5' and/or 3' untranslated regions have optimized expression levels and tissue-specific expression. The methods are used for introns, optimized correction of consensus splice sites, addition of cytoplasmic RNA accumulation. Hence the DNAs are useful in gene therapy regulation. The present sequence represents the full length factor VIII protein encoding gene sequence from the first of the sequence represents the full length factor VIII protein encoding gene sequence from the contents and the contents and contents and contents and contents and contents and contents sequence represents the full length factor VIII protein encoding gene and contents and con
                                                protein encoding gene sequence (construct pLZ-6). This contains an
                                          intron spanning the beta-domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 101-115; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes and vectors exhibiting increased expression and novel splicing patterns, useful for expression of, e.g. beta-domain deleted factor
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05-DEC-1997;
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97US-0067614.
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Sequence 11846 BP; 3419 A; 2718 C; 2607 G; 3102 T; 0 other:

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Matches
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                                                                                                                                                                                                                                                                                                               AAX82260;
                                                                                                                                                                                                                                                                                                                                           AAX82260 standard; cDNA; 12022 BP
                                                                                                                                                                                                             Factor VIII protein; gene modification; gene therapy; clinical disorder; splicing pattern; RNA processing; gene regulation; beta-domain; human;
                                                                                                                                                                                                                                                         Factor VIII protein encoding gene sequence.
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                                                                                                                                                                                                                                                                                    (first entry)
                              /number= 1
3295..6152
                                                                                      /product= "Factor VIII protein"
/note= "contains introns"
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Best Local Similarity
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05-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The method, DNA sequences and expression vectors can be used to increase the expression of a gene, especially a Factor VIII gene. Genes containing modified 5' and/or 3' untranslated regions have optimized expression modified 5' and/or 3' untranslated regions have optimized expression. The methods are used for identification and correction of consensus splice sites, addition of introns, optimization of 5' and 3' untranslated regions and increase in introns, optimization of 5' and 3' untranslated regions and increase in the cytoplasmic RNA accumulation. Hence the DNAs are useful in gene therapy to treat a clinical disorder, to study RNA processing and/or gene regulation. The present sequence represents the gene comprising the regulation contains an intron spanning the portion of the gene encoding the better the contains an intron spanning the portion of the gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes novel genes and vectors exhibiting increased expression and novel splicing patterns. It provides a gene encoding a factor VIII protein, that comprises one or more consensus or near consensus splice sites which have been corrected to increase expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Page 89-100; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genes and vectors exhibiting increased expression and novel splicing patterns, useful for expression of, e.g. beta-domain deleted factor
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                                                                                                                                                                                                                                                                                                                                                                             1001 ccaccatggaaatagagctctccacctgcttctttctgtgccttttgcgattctgcttta 1060
                                                                                                                                                                                                                                                                                                    1061 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 1120
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1181
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                                                                        1241 acatcgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgagg
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                                                                                                                                                                     602 tcaacacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttca 661
                                                                                                                                                                                                                                                                                                                         gtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtg 541
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This cDNA encodes the beta-domain deleted SQN deletion protein of human factor VIII. This is used in the construction of recombinant retroviral vectors expressing human factor VIII. The invention provides the preparation of replication defective recombinant retrovirus (RRV) expressing a therapeutic protein. The RRV preparation is resistant to degradation by human complement and is capable of inducing long term systemic expression of the therapeutic protein when administered intravenously to a human. The long term systemic expression results in a measurable level of the therapeutic protein being produced in the blood of the human for a period of at least 30 days after the administration o
                                                                                                                                                                                                                     New replication defective recombinant retro-viruses - which can be administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable
                                                                                                                                                                             Example 28; Pages 210-213; 272pp; English.
                                                                                                                                                                                                                                                                                                 P-PSDB; AAW46246
                                                                                                                                                                                                                                                                                                                                             Jolly DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Replication defective; Becombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; human; hepatitis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; diabetes; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; hypopituitarism; adenine deaminase deficiency, HIV infection; anaemia; Guacher's syndrome; high blood pressure; Alzheimer's disease, autoimmune; inflammatory disease; factor VIII; ss.
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96US-0645601.
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DC, Ibanez CE;
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Factor VIII; blood clotting; haemophilia A; gene therapy;

vector; human; ss

retrovirus;

Human Factor VIII SQN deletion mutant DNA.

(first entry)

AAV15338 ID AAV1

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AAV15338 standard; DNA; 4832 BP

AAV15338; 20-JUL-1998

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611 tgtggacctggtaaaagacttgaattcaggcctca 645
                     966 tgtggacctggtaaaagacttgaattcaggcctca 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the RRV vector preparation. RRV's can be used for in vivo delivery of therapeutic protein to treat, e.g. haemophilia A, haemophilia B, thrombosis, hypercoagulable disorders, liver diseases such as hepatitis, disorders such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, severe combined immunodeficiency (SCID), cystlc fibrosis, Duchenne's Muscular Dystrophy, inherited emphysema, familial hypercholesterolemia, Muscular hypopituitarism, adenine deaminase deficiency, alphalantitrypsin deficiency, Guacher's syndrome, anaemia, infections such as antitrypsin deficiency, Guacher's syndrome, anaemia, infections such as inflammatory disease or graft versus host disease. RRV's are capable of surviving inactivation in human serum thereby allowing efficient gene
                                                                                               906 gaaaggaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca
                                                                                                                                                    491 ggagaaagaagatgataaagtottccctggtggaagccatacatatgtctggcaggtcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocal Similarity
                                                                                                                                                                            99agaaagaagatgataaagtottoootggtggaagccatacatatgtotggcaggtoot
                                                                                                                                                                                                                                                        tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
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Pred. No. 1.9e-155;
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03-JUL-1996;
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P-PSDB; AAW44372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This DNA sequence includes a coding region for the B domain deletion mutant SQN (see AAW44372) of human Factor VIII. The SQN mutant is created by fusing Ser-743 to Gln-1638 of native Factor VIII (see AAW44373) to form a Ser-Gin-Asn (SQN) link between the A2 viii (see AAW44373) to form a Ser-Gin-Asn (SQN) link between the A2 and A3 Factor VIII domains. When compared to plasmid-derived and A3 Factor VIII domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New replication defective recombinant retroviruses - which express B domain-deleted human factor VIII or human factor IX for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jolly DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                               pharmacokinetics, but the reduced size of the molecule appears to pharmacokinetics, but the reduced size of the molecule appears to decrease proteolytic degradation. The invention relates to preparations of replication defective recombinant retrovirus (RV) preparations and desired human factor VIII protein, where the expressing a B domain-deleted human factor VIII protein, where the recombinant RV is capable of infecting human cells, is resistant to degradation by human complement and is capable of inducing to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administered to a haemophilia A patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 174-175; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of haemophilia
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4832 BP; 1381 A; 1089 C; 1055 G; 1307 T; 0 other;
                                                                                                                                                                                                                                                 426 catgcaaatagagctctccacctgcttctttctgtgccttttgcggattctgctttagtgc 485
                                                                                                                546 cggtgagctgcctgtgggcgcaagatttcctcctagagtgccaaaaatcttttccattcaa 605
                                                                                                                                                                 131 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 190
 666 cgctaagccaaggccaccct@gatgggtctgctaggtcctaccatccaggctgaggttta 725
                                251 cacctcagtcgtgtacanaagactctgtttgtagaattcacggatcaccttttcaacat 310
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                                               cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barber JR, BC
D, Depolo NJ,
                                                                                                                                                                                                                                                                                                       Conservative
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96US-0696381.
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                                                                                                                                                                                                                                                                                                       57.5%; Score 575; DB 19; 1
100.0%; Pred. No. 1.9e-155;
rative 0; Mismatches 0;
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NJ, Greengard J, Hsu DC, Ib
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respess JG;
                                                                                                                                                                                                                                                                                                                                                   Length 4832;
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AAT03571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT03571 standard; cDNA; 6300 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Factor-VIII; blood clotting; haemophilia A; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor-VIII cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
A human liver cDNA sequence (AAT03571) in expression vector pCLB89 encodes the Factor-VIII precursor (see AAR86863). The cDNA was subjected to loop-out mutagenesis and used in the construction of ectors utilised in the transformation of e.g. COS, CHO and C127
                                                                                                                                                                                          deficiency, esp. haemophilia A
                                                                                                                                                                                                                        New deletion mutant of factor VIII - useful for treating factor VIII
                                                                                                                                                                                                                                                                                    P-PSDB; AAR86863
                                                                                                                                                                                                                                                                                                                                                                  pannekoek H,
                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMO ) IMMUNO AG.
                                                                                                                                          Example 1; Fig 1; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 490
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                                                                                                                                                                                                                                                                                                                                                                     Van Leen RW, Van Ooyen AJJ, Verbeet MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87EP-0201121.
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/note= "the sequence is incomplete since it encodes only amino acids 1-2079 of mature Factor-VIII"
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Matches Query Match

Local 575;

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Factor VIII; blood clotting disorders; ss.
                                                                                                                                                               Factor VIII cDNA insert of pCLB89
                                                                                                                                                                                                                                                      AAN81439 standard; cDNA; 8241 BP.
                                                                                                                                                                                                                                                                                                                           546 tgtggacctggtaaaagacttgaattcaggcctca 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666 cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mammailan cells, or Bacillus or Kluyveromyces microbial cells, for prodn. of a Factor-VIII derivative useful in the treatment of haemophilia A. The Factor-VIII derivative has the formula NR-LR-CR, where NR is amino acids 1-712 of Factor-VIII, LR is a short peptide (AAR86864), and CR is amino amino acids 1638-2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6300 BP; 2026 A; 1340 C; 1323 G; 1611 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    catgcamatagagetetecaectgettetttetgtgeetttttgcgattetgetttagtge 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                              /product=factor VIII
                                                  /*tag=
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.5%; Score 575; DB 17; 1
100.0%; Pred. No. 2.1e-155;
tive 0; Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 575;
366 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag
                                                                                                                                726 tgatacagtggtcattacacttaagaacatggcttccccatcctgtcagtcttccatgctgt 785
                                                                                                                                                                                            666 cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725
                                                                                                                                                                               246 cgctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta
                                                                                                                                                                                                                                         186 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 245
                                                                                                                                                                                                                                                        606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                                                                                                                                                                                                                                   546 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa
                                                                                                                                                                                                                                                                                                    126 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8241 BP; 2625 A; 1759 C; 1703 G; 2154 T; 0 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The cDNA was prepd. from human liver RNA. Clone pCLB89 was produced by combining inserts from several positive clones isolated from the cDNA library. The sequence can be inserted into expression vectors for the prodn. of recombinant factor VIII. The protein produced is useful for treating blood clotting
                                                                                                                                                                                                                                                                                                                                                                             486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                                                                                                                                                                                                                                                                      426 catgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgctttagtgc 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression system for producing factor VIII polypeptide in microbial cells - contg. open reading frame and functional
                                                                                                                                                                                                                                                                                                                                                             66 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation and termination regions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (KONN ) GIST-BROCADES NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                      6 catgeaaatagageteteeacctgettetttetgtgeettttgegattetgetttagtge 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUL-1987;
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64..7059
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100.0%; Pr
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100.0%; Pred. No. 2.4e-155;
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AAN81439 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAN81096;
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                                                                                                    The isolation of Factor VIII mRNA from human liver, and the preparation, purification and identification of cDNA and its assembly in the plasmid purification and identification of cDNA and its assembly in the plasmid period to the control of the scalar preparation of plasmid period have been described in patent prollude deletion mutant proteins of Factor VIII polypetides of the invention region or "B domain" as well as a portion of the 92 kD region has been deleted. The polypetides have enhanced Factor VIII activity and/or deleted. The polypetides have enhanced factor VIII activity and/or decreased immunogenicity and can be used for the treatment of decreased immunogenicity and can be used to prepare antibodies. The Abs. Haemophilia A. They can also be used to prepare antibodies. The Abs. can be used to determine the concn. of Factor VIII in a body fluid. Sequence 8241 BP; 2625 A: 1759 C; 1703 G; 2154 T; 0 other;
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US-09-364-862-13
SOFTWARE: PatentIn Ver.
SEQ ID NO 13
LENGTH: 11933
                                           CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
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Patent No. 6221349
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APPLICANT: COLOSI, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
FILE REFERENCE: AVIGEN-03743
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                                             OTHER INFORMATION: Description of Artificial Sequence:
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APPLICANT: COUTO, Linda B.

APPLICANT: Colosi, Peter C.

ITITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII

TITLE OF INVENTION: by Target Cells

FILE REFERENCE: Avigen-04082

CURRENT APPLICATION NUMBER: US/09/470,618

CURRENT FILING DATE: 1999-12-22

EARLIER APPLICATION NUMBER: 09/364,862

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER FILING DATE: 1999-03-24

EARLIER FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 actaggggttoctgcggccgcccagggaatgtttgttcttaaataccatccagggaatgt 180
                                     243 gcagtagtcgccgtgaacgttctttttcgcaacgggtt-----tgccgccccg 290
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                                                                                                                                     301 aggcaggtaagtgccgtgtgtgggttcccgcggggcctggccttttacgggttatggccct 360
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                                                                                                                351 tottaaataccatctactgacactgacatccactttttcttttttctccacaggtatcga- 409
                                                                                                                                                                                           291 cggcaggtaagtgccagggaatgtttgttcttaaataccatcgctccagggaatgtttgt 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 72.5%; Score 725.2; DB 4; Local Similarity 85.9%; Pred. No. 1e-220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 cagetgegegetegetegeteaetgaggeegeeegggeaaageeegggegtegggegaee 60
                                                                                                                                                                                                                                                                                                                                                   gatgtcgtgtactggctcc---gcctttttccccgagggtgggggagaaccgtatataagt 242
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agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 540
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US-09-364-862-14
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic \textsc{US-09-364-862-14}
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                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Colosi, Peter C.
                                                                                                         Matches
                                                                                                                        Best Local
                                                                                                                                     Query Match
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 agtgccaccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagt 529
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61 tttggtcgcccggcctcagtgagcgagcgagcgcgcagagagggagtggccaactccatc 120
                                   13 cagctgcgcgctcgctcactgaggccgccggggcaaagcccgggcgtcgggcgacc 72
                                                  1 cagctgcgcgctcgctcgctcactgaggccgcgggcaaagcccggggcgtcgggcgacc
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                                                                                                                          Similarity
                                                                                                             Conservative
                                                                                                                            72.5%;
                                                                                                             0; Mismatches 118; Indels 23; Gaps
                                                                                                                            Score 725.2; DB pred. No. 1e-220;
                                                                                                                                                  DB 4; Length 4999;
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Sequence 1, Application US/08882083
Patent No. 5869292
GENERAL INFORMATION:
APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                   US-08-882-083-1
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      APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                950 tctcatgtggacctggtaaaagacttgaattcaggcctca 989
                                                                                                                                                                                                                       961 tctcatgtggacctggtaaaagacttgaattcaggcctca 1000
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 578;
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390 CTGTTGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTC
                                                                                 782 ctgttggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtc
                                                                                                                                           722 tttatgatacagtggtcattacactttaagaacattggcttcccatcctgtcagtcttccatg
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/558,107
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      150 ATCTCGGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                     482 gtgccaccagaagatactacctgggtgcagtggaactgtcatgggaactatatgcaaagtg 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                  90 GTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGGACTATATGCAAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                               30 CCACCATGGAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTGCGATTCTGCTTTA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Foley
STREET: 3000 K St
CITY: Washington
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                                                                                                                            TTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATG
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(202)672-5399
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SYSTEM: PC-DOS/MS-DOS
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99.8%;
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; LOCATION:
US-08-558-107-1
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patent No. 5910481
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: VOORBERG, Johannes J.
                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,715
REFERENCE, POCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5390
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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                                                                                                                                                      APPLICATION NUMBER:
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TELEX: 904136
                                                                                                    150 ATCTCGGTGAGCTGCGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCAT 209
                                                                 542 atctcggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccat 601
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602 tcaacacctcagtcgtgtataaaaagactctgtttgtagaattcacggatcaccttttca 661
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3000 K Street, N.W., Suite 500
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99.8%;
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LOCATION:
US-09-243-539-1
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                                                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 902 tcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatcttt 961
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                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
REGISTRATION NUMBER: 33,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300
                                                                                                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                         FEATURE:
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                         APPLICATION NUMBER: US UF TILING DATE: 13-NOV-1995
                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                            TELEFAX:
                                                    TOPOLOGY:
                            NAME/KEY:
                                                                                         LENGTH:
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3000 K Street, N.W., Suite 500
                                                                                             5035 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                (202)672-5399
                                                       linear
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Query Match

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PATENT NO. 5171844

APPLICANT: VAN OOYEN, ALBERT J.J.; PANNEKOEK, HANS; VERBEET, MARTINUS P.: VAN LEEN, ROBERT W.
TITLE OF INVENTION. PROTEINS WITH FACTOR VIII ACTIVITY PROCESS FOR THEIR PREPARATION USING GENETICALLY-ENGINEERED CELLS AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM NUMBER OF SEQUENCES: 12.
NUMBER OF SEQUENCES: 12.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          5171844-1
                                                                                                                                                                                                                                                                                           ; SEQ ID NO:1:
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                                                                                                                                                                     Matches 575;
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                           486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                            426 catgcaaatagagctctccacctgcttctttctgtgcctttttgcgattctgctttagtgc 485
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         66 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 125
                                                                          6 catgeaaatagageteteeacetgettetttetgtgeetttttgegattetgettlagtge 65
                                                                                                                                                                                                                                                                         LENGTH: 8241
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                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                  FILING DATE: 10-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 TCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACCTTACCTCATATCTTT 569
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                                                                                                                                                               Conservative
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                                                                                                                                                   57.5%; Score 575; DB 6; L6
100.0%; Pred. No. 9.2e-173;
ative 0; Mismatches 0;
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90.88;
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                                                           TELEFAX: (619) 452-2616
INFORMATION FOR SEQ ID NO:
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                           SEQUENCE CHARACTERISTICS:
LENGTH: 8967 base pairs
                                                                                                              REFERENCE/DOCKET NUMBER: 34,561
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,851A
                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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STREET: San Diego
CTATE: California
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                   TYPE:
STRANDEDNESS:
                                                                                                TELEPHONE:
                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                       NAME:
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546 tgtggacctggtaaaagacttgaattcaggcctca 580
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                nucleic acid
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11055 Roselle
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SYSTEM: PC-DOS/MS-DOS
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US-08-366-851A-1
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US-07-864-004B-3
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                                                                                                                                                      Sequence 3, Application US/07864004B patent No. 5364771
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                            Match 57.5%; Score 575; DB 1; Local Similarity 100.0%; Pred. No. 9.6e-173; Local S75; Conservative 0; Mismatches 0;
                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                 409 TGATACAGTGGTCATTACAGTTAAGAACATGGGTTTCCCCATCCTGTCAGTCTTCATGCTGT 468
                                                                                                                                                                                                                                                                                                                                                                                 726 tgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgt 785
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                 APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor
                                                                                                                                                                                                                                 966 tgtggacctggtaaaagacttgaattcaggcctca 1000
COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: FOR PC-DOS/MS-DOS
                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                649 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 683
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                                                                   STREET: 1100
CITY: Atlanta
                                                 COUNTRY:
                                                                                       ADDRESSEE:
                                                                                                                                                INFORMATION:
                                         30309
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1100 Peachtree Street
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US-07-864-004B-3
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Best Local Similarity
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: ENTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5001 . . 7053
OTHER INFORMATION: /note= "Equivalent to to THER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                   426 catgcaaatagagctctccacctgcttctttctgtgccttttgcgattctgctttagtgc 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE:
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                                                                                                                                                                                                                                                     210 CACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 269
                                                                                                                                                                                                                606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                 666 ogotaagocaaggocacoctggatgggtotgotaggtoctacoatcoaggotgaggttta 725
                                                                                                                                                                                                    330 CACCTCAGTCGTGTACAAAAAGACTCTGTTTGTAGAATTCACGGTTCACCTTTTCAACAT 389
                                                                                                                                                   390 CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTA 449
510 TGGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAG 569
                                                             786 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
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                                                                                                                                                                                                                                                                                                                                                                                                                           57.3%; Score 573.4; DB 1; Length 9009; 99.8%; Pred. No. 3.1e-172;
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US-08-251-937A-3
     Best Local Similarity
                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-4992
ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S
REGISTRATION NUMBER: 29,476
REGISTRATION NUMBER: 29,476
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INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     MOLECULE NO
                                                                                                                                                      OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08251937A Patent No. 5583209
                                                                                                                                                                                                                                                                      FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                        OTHER INFORMATION: /note= "Equivalent to the Al-A2 OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PACE.....
SOFTWARE: PACE.....
CURRENT APPLICATION NUMBER: US/Q$/251,937A
APPLICATION NUMBER: 31-MAY-1994
                                                                                                      NAME/KEY: misc_feature (Domain Structure)
LOCATION: 1 2277
                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                      NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5001 . . . 7053
                                                                                                                                                                                                                                          TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOllar, John S. APPLICANT: Runge, Marschall S. TITLE OF INVENTION: Hybrid Hun
                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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OPERATING SYSTEM:
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C: US
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1100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                    linear
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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O
                                                                                                                                                                                                                                                                                                                                     CDNA
                                                                                                                                                                                                                                                                                                                                                                 single
     57.38;
99.88;
                                                                                                                                                      /note= "Equivalent to the A3-C1-C2 domain"
Pred. No. 3.1e-172;
             Score 573.4; DB 1;
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        Length 9009;
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RESULT 12
US-08-212-133A-1
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Patent No. 5663060
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    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                           COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                    APPLICANT: Lollar, John S. APPLICANT: Runge, Marschall S. TITLE OF INVENTION: Hybrid Hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 574; Conservative
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                     APPLICATION NUMBER: US/08/212,133A FILING DATE: March 11, 1994
                                                                                                                                                                                                                        STREET: 100 P
                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 690 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 CÓGTGAGCTGCCTGTGGACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 cggtgagctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaa 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
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Pabst, Patrea L.
                                                                                                                                                                                                    Georgia
(: US
                                                                                                                                                                                                                                                                                                                                                       _Application US/08212133A
                                                                                                                                                                                                                                    100 Peachtree Street
                                                                                                                                                                                                                                                  Kilpatrick & Cody
                                                                                                                                                                                                                                                                                Hybrid Human/Animal Factor VIII

 Mismatches

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TELECOMMUNICATION INFORMATION: TELEPHONE: 404-572-6508

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMI

EMU/76677

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US-08-212-133A-1
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Best Local Similarity 99.8%;
Matches 574; Conservative
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INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5125 7053
OTHER INFORMATION: /note= "Equivalent to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                               TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                               486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                   606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                                                                                                                            NAME/KEY:
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                                                                                                      SENSE:
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                                                                                                                                                                                                                                                                                                                                                                           /note= "cDNA encoding human factor VIII."
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domain"
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 Mismatches

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US-08-474-503-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Hybrid Human/Animal Factor VIII NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                   Query Match 57.3%;
Best Local_Similarity 99.8%;
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                                                        Matches 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: pratt, John S.
REGISTRATION NUMBER: 29,476
REFERENCE/DOCKET NUMBER: EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6500
                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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CITY: Atlanta
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                                                                                                                                LOCATION: 1..2277
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5125 . . 7053
OTHER INFORMATION: /note= "Equivalent to tother Information: domain"
                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                  TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                         NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 . . . 2277
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                                                             Conservative
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                                                                                                                                              /note= "cDNA encoding human factor
VIII."
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                                                                0; Mismatches
                                                                            Score 573.4; DB 1; Length 9009; pred. No. 3.1e-172;
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US-08-670-707A-1
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                                                              APPLICATION NUMBER: WM PCT
FILING DATE: 15-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08670707A Patent No. 5859204
GENERAL INFORMATION:
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             FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy, disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/WS-DOS

SOFTWARE: Patentin-Re-lease #1.0, Version #1.30
                                                   PRIOR APPLICATION DATA:
                                                                                                                                  PRIOR APPLICATION DATA: ":
                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Greenlee, Whomer and Sullivan, P.C.
                       APPLICATION NUMBER: US 0
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lollar, John S. TITLE OF INVENTION: Hybrid
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                          APPLICATION NUMBER: US/08/670,707A FILING DATE: 26-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              690 TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            966 tgtggacctggtaaaagacttgaattcaggcctca 1000
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Greenlee, Lorance L.
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                                                                                                                                                                                                                                                                                       USA
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                                   US 07/864, 004
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US-08-670-707A-1
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906 gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
                                          510 TEGTGTATCCTACTGGAAAGCTTCTGAGGGAGCTGAATATGATGATGACCAGTCAAAG 569
                                                                                                                  786 tggtgtatcctactggaaagcttctgagggagctgaatatgatgatcagaccagtcaaag 845
                                                                                                                                                                            726 tgatacagtggtcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgt 785
                                                                                                                                                              450 TGATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGT 509
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                                                                                                                                                                                                                                       666 ogctaagccaaggccaccctggatgggtctgctaggtcctaccatccaggctgaggttta 725
                                                                                                                                                                                                                                                                                330 CÁCCTCÁGTGGTGTÁCAAAAAGACTCTGTTTGTÁGAATTCACGGTTCACCTTTTCAACAT 389
                                                                                                                                                                                                                                                                                               606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                                                                                                                                                                                                                                                        TELEFAX: 303/499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   210 CÁCCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCT 269
                                                                                                                                                                                                                                                                                                                                                                                                                  486 caccagaagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatct 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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OTHER INFORMATION: /note= "cDNA encoding human factorVIII"
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REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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OTHER INFORMATION: /note= "Equivalent to the A3"
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Lollar, Wohn S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPOTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630 GAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCA 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 11-MAR-PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ferber, Donna M. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/864,004 FILING DATE: 07-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0: FILING DATE: 11-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: WO POFILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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                                                                               NAME/KEY: misc_feature LOCATION: 1..2277
OTHER INFORMATION: /pro
                                                                                                                                              OTHER INFORMATION: /product= "Domain Structure" OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2 domain"
                                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 5125..7053
                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                             OTHER INFORMATION: /note= "Equivalent to the A1-A2 domain"
                                                                                                                                                                                                                               TISSUE TYPE:
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              NAME/KEY: misc_feature LOCATION: 1..2277
OTHER INFORMATION: /product= "Domain"
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26-JUN-1996
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                                                                                /product= "Domain Structure"
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; OTHER INFORMATION: /note= "cDNA encoding human factorVIII" US-09-037-601-1
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                                                                                                                                                                                                                                                         606 cacctcagtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacat 665
                                                                                                          726 tgatacagtggtcattacacttaagaacatggcttcccatcctqtcagtcttcatgctgt 785
        966 tgtggacctggtaaaagacttgaattcaggcctca 1000
                                  TGTGGACCTGGTAAAAGACTTGAATTCAGGCCTCA 724
                                                   gaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctttctca 965
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Search completed: January 8, 2002, 17:19:07 Job time: 12198 sec

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Minimum DB seq length: 0
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score greater than or equal to the score of the result being printed,
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AK014835
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BG477974 602522966
AA817854 UI-R-A0-a
BF150467 uy86b07 y
AA461838 vf95404 r
A1526753 uj42-03 y
BG92386 60284575
BG927142 602846744
BE912296 601666013
AK014835 Mus muscu
A1225600 uj06c05 y
AA865338 og88d10 s
AL556703 AL556703
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ALIGNMENTS

RESULT

	source	FEATURES							COMMENT	AL			REFERENCE		ORGANISM I	SOURCE	S		ACCESSION 1		ITION		BG477974
/Organism="homo sapiens /db_xref="haxon:9606" /clone="IMAGE:4641352" /clone_lib="NIH_MGC_20" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)"	1954	High quality sequence stop: 626. Location/Qualifiers	http://image.lini.gov Plate: LLCM1408 row: c_column: 17	found through the I.M.A.G.E. Consortium/LLNL at:	DNA Sequencing by: Incyte Genomics, inc. Clone distribution: MGC clone distribution information can be	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Preparation: Ling Hong/Rubin Laboratory	missue Produrement: ATCC/DCTD/DTP	Contact: kopert strauspery, fm.v.	Unpublished (1999)	National Institutes of Health, Mammailan Gene Correction (MOC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 954)	Eukaryota; Metazoa; Chordata; Cranidid; Velicuides, Eucaroscomos Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens	human.	EST.	BG477974.1 GI:13410253	BG477974	πRNA sequence.	602522966F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4641352 5',	BG477974 954 bp mRNA EST 21-MAR-2001	

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REFERENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                        AA817854 456 bp mRNA DI-R-AO-ae-g-10-0-UI.S1 UI-R-AO Rattus norvegicus cDNA clone UI-R-AO-ae-g-10-0-UI 3' similar to gb|L33869|RATCERU Rat norvegicus
            Contact: Soares, MB Program for Rat Gene Discovery and Mapping
                                                          On Mar 9, 1998 this sequence version replaced gi:2946779
                                                                                         discovery .
Genome Res 6 (9), 791-806 (1996)
University of ·Iowa
                                                                                                                                                      Normalization and subtraction: two approaches
                                                                                                                                                                                 l (bases 1 to 456)
Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                          GI:4198380
                                                                                                                                                                                 Lennon, G. and Soares, M.B.
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89.0%;
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                                               uy86b07.y1
similar to
BF150467
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Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Ovary library. cDNA Library Preparation: M. Fatima Bonaldo, Ph.D. Clone distribution: clones will be available through Research Genetics This clone is also available through the I.M.A.G.E. Consortium at LDNL (info@image.lln1.gov). IMAGE ID=1767329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B (Life Technologies)"
/note="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; This library consists of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, bra liver, kidney, heart, spleen, ovary, and muscle. The tis a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification the library of origin of a clone within the mixture."

a 105 c 101 g 144 t
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/clone_lib="UI-R-A0"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                       NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666421 5' SW:CERU_MOUSE Q61147 CERULOPLASMIN PRECURSOR ;, mRNA
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979 aaagacttgaattcaggcctca 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 270
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                                              CCTGGAGAGGGAGACAGCAATTGTGTGACCAGGATNTACCACTCCCATGTTGATGCTCNC 567
                                                                        ccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggta 978
                                                                                                                                                                       gataaagtottoootggtggaagooatacatatgtotggcaggtootgaaagagaatggt 918
                                                                                                                                                                                                                                               tggaaagcttctgagggagctgaatatgatgatcagaccagtcaaagggagaaagat 858
                                                                                                                                                                                                                                                                                                                                                                                                    CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 330
                                                                                                                                                                                                                                                                                                                                                                                                                           ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                                                                    GACAAAGTGCTTCCCGGACAACAGTATGTGTATGTGCTGCATGCC---AATGAGCCAAGT 507
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Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 669)
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
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Similarity 54.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/db xref-":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:3666421"
/clone_lib="NCI_CGAP_Mam5"
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Pred. No. 2.4e-16;
0; Mismatches 172;
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137 CCAGCCTGGCTTAGGGCTTTTAGGCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 196
                      679 ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                                                                  619 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 678
                                                                                                                                                                                                         Local
                                                                                          TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                                                                                                                     208;
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vf95d04.r1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:851527 5' similar to gb:M13699 CERULOPLASMIN PRECURSOR (HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                            148 a
                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                           adaptors (Pharmacia), digested with Not I and cloned int
the Not I and Eco RI sites of the modified pTTT3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st_strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:851527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares_mammary_gland_NbMMG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
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54.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               double-stranded cDNA was ligated to Eco RI s (Pharmacia), digested with Not I and cloned into
                                                                                                                                                                                        0; Mismatches 171;
                                                                                                                                                                                                           Score 92.4; DB 10; Length 477; Pred. No. 2.4e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI526753 625 bp mRNA EST 18-MAR-1942603.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1922620 5' similar to gb:M13699 CERULOPLASMIN PRECUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium finfo@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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314 286 1810
/note="organ: liver; Vector: pME18S-FL3; Site_1: DrailI (CACTGTGTG); Site_2: DrailI (CACCATGTGTG); 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTTTTT); double-stranded cDNA was ligated to a DrailI adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DrailI sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library
                                                                                                                                                                                                                                                                                          /clone_lib="Sugano mouse liver mlia"
/sex="female"
                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                  /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                              /db_xfef="taxon:10090"
                                                                                                                                                                                                                                                                                                                                      /clone*"IMAGE:1922620"
                                                                                                                                                                                                                                                                                                                                                                                             /strain*"C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus
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                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10912 row: j column: 22
                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                     High quality sequence stop:
                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 658)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG923886 658 bp mRNA EST 05-JUN-2001 602884585E1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4953333 5',
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                                    /organism="Mus musculus"
/db_xref="taxon:10090"
                  /strain="FVB/N"
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                                                            .658
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Pred. No. 2.7e-16;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468 GACAAAGTGCTTCCCGGACAACAGTATGTGTATGTGCTGCATGCC---AATGAGCCAAGT 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           408 ACCAAGGAGTATGAGGGAGCCGTCTACCCTGACAACACCACTGATTTTCAACGGGCTGAT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                739 attacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctac 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccamtggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggta 978
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; So
1 (bases 1 to 783)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG977142 783 bp. mRNA EST 12-JUN-2001
602846744F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4977442 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG977142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG977142.1 GI:14364779
                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                  Unpublished (1999)
                                                                                                                                                                                                                                                      National Institutes of Health, Mammalian Gene Collection (MGC)
                 found through the-I.M.A.G.E. Consortium/LLNL http://image.llnl.gov
                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                   CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
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row: g column: 11
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Mismatches 171;
                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Musinae;
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                                                                JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCAAAGCTGAAGTTGAAGATAAAGTTTAT 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC 435
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                        601666013F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3966051 5',
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                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 878)
                                                                                                                                                                                                                                                            BE912296.1 GI:10409387
                                                                                                                                                                                                                                                                                                     mRNA sequence.
                                         Contact: Robert Strausberg, Ph.D.
                                                           Unpublished (1999)
Tissue Procurement: Gilbert Smith, Ph.D
                                                                                                                                                                                                                   house mouse
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                         cgapbs-r@mail.nih.gov
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161 c 176 g 210 t
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/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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/strain="FVB/N"
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Pred. No. 2.9e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                       Mus musculus
                                                                                   CAP trapper.
Mus musculus (strain C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
                                                                                                                                                                                                                                        Mus musculus adult male testis cDNA, RIKEN full-length enriched
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                           clone:4921507J22.
                                                                                                                                                                         AK014835.1 GI:12652907
                                                                                                                                                                                                                                                                              AK014835
                                                                                                                                                                                                                    library, clone:4921507J22, full insert sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 a
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
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                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arakawa, T., Carninci, P., Fukuda, S., Fukudishi, Y., Furuno, M.,
Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F.,
Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kato, H., Kawal, J.,
Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Kijima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T.,
Kijima, Y., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y.,
Okido, T., Owa, C., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H.,
Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A.,
Yoshino, M., Muramatsu, M., and Hayashizaki, Y.
Direct Submission
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Nature 409, 685-690 (2001)

5 (bases 1 to 3739)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, Adachi, J., Carninoi, P., Fukuda, S., Fukunishi, Y., Furuno, M., Garninoi, P., Fukuda, S., Fukunishi, Y., Garninoi, P., Garni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              further details.
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High-efficiency full-length cDNA cloning
Methods in enzymology. 303, 19-44 (1999)
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208;
                                                                                WashIngton Uniwersity School of MedicineP
Washington Uniwersity School of MedicineP
4444 Forest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI225600 1006 bp mRNA EST 29-OCT-1998 uj06c05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1891112 5' similar to gb:M13699 CERULOPLASMIN PRECURSOR
  This clone is available
                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                           The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                         Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T. Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMAN);, mRNA sequence.
AI225600
AI225600.1 GI:3808653
                                                                                                                                                  Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                         Waterston, R
                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1006)
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                      mouseest@watson.wustl.edu
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/tissue_type="testis"
/tissue_type="RIKEN full-length enriched mouse cDNA library"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
768 c 821 g 995 t 1 others
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/db_xref="MGD:MGI:88476"
/clone=14921507J22"
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Pred. No. 5e-16;
Pred. No. 5e-16;
royalty-free through
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sequence.
AA865338
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                                                                                                                                 AA865338 521 bp mRNA EST 29-APR-1998 og88d10.s1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1455379 similar to gb:M13699 CERULOPLASMIN PRECURSOR (HUMAN);, mRNA
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 4.1e-16;
0; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 TATATAAGAAGGCCCTTTATCTTCAGTACACAGATGAAACCTTTAGGACAACTATAGAAA 366
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              977 taaaagacttgaattcaggcctca 1000
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                                                                                                                                                                     atgataaagtetteeetggtggaageeataeatatgtetggeaggteetgaaagagaatg 916
                                                                                                                                                                                                                                                                                                                                                                                                      ggccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtgg 736
                                                                                        gtccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctgg
                                                                                                                                                                                                                                                                                                                                                                                 AACCGGTCTGGCTTTGGGTTTTTAGGCCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT
                                                                                                                                                                                                                                                                                                 tcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcct 796
                                                    GTCCTGGGGAAGGAGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC
                                                                                                                                                                                                                   ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG
                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 656     Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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h quality sequence stop: 360.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:1455379"
/clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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82.33; Pred. No. 5.7e-16;
tive 0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 521;
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                                                                                                                                                               857
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                                                                                                                                                                                                                            AACCGGTCTGGCTTTTTTAGGCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT 318
                                                                       gtccaatggcctctgacccactgtgccttacctactcatatctttctcatgtggacctgg 976
                                                                                                                                          atgataaagtottoootggtggaagcoatacatatgtotggcaggtootgaaagagaatg 916
                                                                                                                       ATGACAAAGTATATCCAGGAGAGCAGTATACATACATGTTGCCTTGCCACTGAAGAACAAA 498
                                                                                                                                                                                                     ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG 438
                                                                                                                                                                                                                                                                                                       tcattacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcct 796
                                         GTCCTGGGGAAGGAGATGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC 558
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Contact: Genoscope
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AL556703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: provision of site_1: NotI; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco Rv sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 169 c 192 g 253 t 1 others
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/db_xref="taxon:9606"
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52.3%;
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859 gataaagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggt 918
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                                                                                                                                                                                                                                                                                                                  210 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTCAGACTATAGACAAA 269
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                                              ACCAAGGAGTATGAGGGAGCCGTCTACCCTGACAACACCACTGATTTTCAACGGGCTGAT 449
                                                                             GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC 389
                                                                                                                                                                 attacacttaagaacatggcttcccatcctgtcagtcttcatgctgtttggtgtatcctac 798
                                                                                                                                                                                                                                                        ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the MJ.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG862595 632 bp mRNA EST 29-MAY-2001 602795978F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4917258 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Library."
185 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2.5 kb. Library constructed by Life Technologias, catalog # 12018-016. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-Ii (1996). Note: this is a NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="IMAGE:4917258"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tumor, gross tissue"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_CGAP_Mam4"
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Pred. No. 7.9e-16;
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383 ACTATAAGGAACATGAGGGGGCCATCTACCCTGATAACACCACAGATTTTCAAAGAGCAG
                        263 AACCGGTCTGGCTTTGGGTTTTTAGGCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT 322
                                                                                                                                                                        677 ggccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtgg 736
                                                                                                                                                                                                                            203 TATATAAGAAGGCCCTTTATCTTCAGTACACAGATGAAACCTTTAGGACAACTATAGAAA 262
                                                                                                                                                                                                                                                               617 tytacaaaaayactctytttytayaattcacygatcaccttttcaacatcyctaayccaa 676
                                                                                                                                                                                                                                                                                                                                 Match 9.0%;
Local Similarity 52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qian,B., Wu,T., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z., Xiao,I., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z., Qu,J., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Chen,Z. and Han,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
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xhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="corresponding non cancerous liver tissue"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCDJA09"
/clone_lib="GLC"
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Pred. No. 1.8e-15;
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                                                                                                                                                                                                                                                         Matches 201;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 443 ATGACAAAGTATATTCAGGAGAGCAGTATACATACATGTTGCCTTGCCACTGAAGAACACA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     857 atgataaagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatg 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              563 CAAAAGATATTGCCTCAGGACTCA 586
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                                                                                                                                                                                           619 tacaaaaagactctgtttgtagaattcacgatcaccttttcaacatcgctaagccaagg 678
333 GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC
                      739 attacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctac 798
                                                                                                        679 ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc 738
                                                                                273 CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 332
                                                                                                                                                                     213 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 272
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BF144665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1. (bases 1 to 8\beta0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM9278 row: f column: 07 High quality sequence stop: 679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                           268 a
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; transgenic model WNT-1, expression driver MMTV-LTR enhancer; Cloned unidirectionally. Primer: OldT. Library constructed by Life Technologies.
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/clone="IMAGE:402202"
/clone_11b="NCI_CGAP_Lu30"
/tissue_type="fumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                      Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="CZECH II"
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                                                                                                                                                                                                                                                                                8.7%;
54.0%;
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Primer: Oligo
             392
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Search completed: January 8, 2002, 15:12:55 Job time: 4771 sec

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Scoring table:
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Maximum DB seq length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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pred. No. is the number of results predicted by chance to have a score greater thap or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

> REFERENCE AUTHORS

TITLE JOURNAL

synthetic construct artificial sequence.

1 (bases 1 to 2297)

Bestetti.G., Cali.S., Orsini.G., Tonon.G., Zuffi.G. and Ghisotti.D. Bestetti.G. cali.S. or the production of natural nucleosides and modified analogues thereof
Patent: WO 0039307-A 11 06-JUL-2000;
BESTETTI GIUSEPPINA (IT); CALI SIMONA (IT); NORPHARMA SPA (IT);
ORSINI GAETANO (IT); TONON GIANCARLO (IT); ZUFFI GABRIELE (IT);

SOURCE

synthetic construct.

ORGANISM

SUMMARIES

FEATURES

GHISOTTI DANIELA (IT)

Location/Qualifiers
1. .2297

source

VERSION KEYWORDS SOURCE	RESULT 1 AX027819/c LOCUS DEFINITION ACCESSION		4.4	43	42	40	39	C 37	36					c 29																æ ~	10	υn 4	<u>م</u>	2	-	Result No.
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                                         TTTCGTCTCGCGCGTTTTCGGTGATGACGGTGAAAAACCTCTGACACATGCAGCTCCCGGAG
                                                        tttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag
                                                                                                 GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                            atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac 780
                                                                                                                                                                                                                                                                                                                                                                                  tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
                                                                                                                                                      ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC
                                                                                                                                                                                                                           caatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgt 720
                                                                                                                                                                                                                                                                                                                                           tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacagggaaggcaaaat 600
                                                                                                                                                                                                                                                                                                                                                                                                                                          CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC 663
                                                                                                                                                                                                                                                                      GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTT
                                                                                                                                                                                                                                                                                     gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                                              TCTTCAGCATCTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT
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574 c 580 g 572 t
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/db_xref="taxon:32630"
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                   agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1040
                                                                                                cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
                                                                        CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-SEP-2000) Waksman Institute, Rutgers Stat
University, 190 Frelinghuysen Road, Piscataway, NJ 0885
Sequence update by submitter
On Oct 3, 2000 this sequence version replaced gi:209216
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (27-APR-1993) Waksman Institute, Rutgers
Submitted (27-APR-1993) Waksman Institute, Rutgers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University, 190 Frelinghuysen Road, Piscataway, 3 (bases 1 to 2368)
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New pUC-derived cloning vectors with different selectable markers and DNA replication origins
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1 (bases 1 to 2368)
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                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/product="beta-lactamase"
/product="beta-lactamase"
/protein_id="AAG18332.1"
/protein_id="AAG18332.1"
/db_xref="c1:10504975"
/translation="mSIQHFRVALIPEFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
/translation="mSIQHFRVALIPEFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSONDLVE
YSPVTEKHLIDGMTVRELCSAAITMSDNTAANLLLTTIGGERELTAFIHNWGDHVTRL
YSPVTEKHLIDGMTVRELCSAAITMSDNTAANLLLTTIGGERELTAFIHNWGDHVTRL
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LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="bla"
513. .1373
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/db_xref="taxon:137702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="multiple cloning site"
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Cloning vector pSP70.
Cloning vector pSP70
Cloning vector pSP70
artificial sequence; v
1 (bases 1 to 2417)
                                                                                      Cloning vector pSP70.x65330
                                                                                                                CVPSP70
                                                              beta-lactamase; bla gene;
                                                                          X65330.1 GI:58235
                                                                                                          2417 bp
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                                                                cloning vector; multiple cloning site;
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1424
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                                                                                                                                                                                                                                                                                                                                                                                                                                       61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                                               tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
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                                                                                                                                                                                                                                                                                                       cgctcgtcgtttggtatggcttcattcagctccggttccccaacgatcaaggcgagttaca 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-MAR-1992) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Technical, Services.
Direct Submission
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In Wisconsin 800-356-9526
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/product="G1-Se236"
/protein_id="G1-Se236"
/db_xref="G1-Se236"
/db_xref="G1-Se236"
/stref="G1-Se236"
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/db_xref="taxon:90135"
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Submitted (28-MAY-1993) Technical Services, Promega 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA See X65300-X65335 for related vector sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | CCacatagcagaactttaaaagtgctcatcattggaaaacgttcttcgggggcgaaaactc 480
                                                                                                                                                                artificial sequence; vectors.
1 (bases 1 to 2419)
Technical Services.
                                                                                                      Submitted (23-MAR-1992) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA
                                                                                                                                                                                                                     Cloning vector psp71. Cloning vector psp71
                                                          Direct Submission
                                                                                       revised by [2]
2 (bases 1 to 2419)
                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                           beta-lactamase; bla gene; cloning vector; multiple cloning
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                                                                       rechnical,Services.
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Best Local Similarity 100.0%;
                                                         1666 GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG 1725
                                                                                                                                                            1606
421 ccacatagcagaactttaaaagtgctcatcatttggaaaacgttcttcggggcgaaaactc 480
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                                                                                 361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                                                                                                      1426 CGCTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Order or Technical 800-356-9526
In Wisconsin 800-356-9526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This vector can be obtained from Promega Corporation, Madison, WI call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    information:
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2402. .2419
/notem"SP6 promoter"
a 601 c 592 g
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/product="Beta-lactamase"
/product="CAAA6431.1"
/protein_id="CAAA6431.1"
/db_xref="GI:58238"
/translation="MsJOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIFNDERDTTMPVAMATTLRKLLTGELLTLASRQQLLDMMEADKVAGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="T7 transcription initiation site complement(1092. .1952) /gene="bla"
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53. .75
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/db_xref="taxon:90136"
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                                                                                                                                                                                                                                                                                                                                              artificial sequence; vectors 1 (bases 1 to 2450)
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                                                                                                                                                                                                                                                                                                                                                                                                                           U74374.1 GI:1649038
                                                                                                                                                                                                                        Submitted (11-OCT-1996) Stanford University, Stanford Human Genome Center, 855 California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                 Fan,J.-B., Quackenbush,J. and Myers,R.M.
pJF5 Cloning Vector
                                                                                                                                                                                                                                                         2 (bases 1 to 2450)
Fan,J.-B., Quackenbush,J. and Myers,R.M.
Direct Submission
                                                                                                                                                            855 California Ave.
Palo Alto, CA 94304 USA.
                                                                                                                                                                                           Stanford Human Genome Center
                                                                                                                                                                                                             Contact: R. M. Myers
                                                                                                                                               Ampicillin Resistance Selectable Vector used in Transposon-Mediated
                                                                                                                                                                                                                                                                                                    Unpublished (1996)
/note="Multiple Cloning Site
XhoI/PvuII/BstXI/XbaI/BamHI/EcoRI/BstXI/EcoRV/BglII"
                                        /note="SP6 transcription initiation site"
                                                                                        organism="Cloning Vector pJF5"
                                                                         /db_xref="taxon:53561"
                                                                                                                     ocation/Qualifiers
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                                                                         IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEOLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTTGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMFVAMATTURKLLTGELLTLASRQQLIDMMEADKVAGPL
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/note="SP6 promoter"
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EIGASLIKHW"
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/translation="MSIQHERVALIPEFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
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/transl_table=11
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100.0%; Pred. No. 1.2e-274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9tctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc 840
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                                                                                                                                                                                                                                                                                Outside U.S
                                                                                                                                                                                                                                                                                                             Order or Technical 800-356-9526
                                                                                                                                                                                                                                                                                                                                      This vector can be obtained from Promega Corporation, Madison, Call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JAN-2000) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA On Jan 26, 2000 this sequence version replaced gi:58239. See X65300-X65335 for related vector sequences
                                                                                                                                                                                                                                                                                                 In Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          revised by [3]
3 (bases 1 to 2462)
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                                                                                                                                                                                                                                                                                                                                    information:
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Cloning vector pSP72.
Cloning vector pSP72
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                      /note="T7 transcription initiation site" complement(1135...1995)
/gene="bla"
complement(1135. .1995)
                                                                                                                      /note="multiple cloning sites"
99. .118
                                                                                                                                                              /note="SP6 transcription initiation site"
                                                                                             /note="T7 promoter"
                                                                                                                                                                                                      /organism="Cloning vector psp72"
/db_xref="taxon:90137"
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s Hollow Road, Madison, Wi 53711-5399, USA
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2069 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGGAAAAGTGCCACCTGAC 2128
                                                                      2009 CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT 2068
                                                                                                                                               1949 GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTT
                   721 atttagaaaataaacaaataggggttccgcgcacatttccccggaaaagtgccacctgac 780
                                                                                                                                                                                                                                                                                        1829 TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA 1888
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                                                                                           661 caatattattgaagcatttatcagggttattgtctcatgagcgggatacatatttgaatgt 720
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                                                                                                                                                                                                                                     541 tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaat 600
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/note="SP6 promoter"
/note=14 c 605 g
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/codon_start=1
/transl_table=11
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/protein_id="CAA46432.1"
/db_xref="GI:58240"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  beta-lactamase; bla gene; cloning vector; multiple cloning site;
                                                                                                                                                                                                                                                                                                                          Submitted (12-JAN-2000) Technical Services, promega Corporation, Submitted (12-JAN-2000) Modison, Wi 53711-5399, USA 2800 Woods Hollow Road, Madison, Wi 53711-5399, USA on Jan 26, 2000 this sequence version replaced gi:58241. See X65300-X65335 for related vector sequences This vector can be obtained from Promega Corporation, Madison, WI. Call one of the following numbers for order or technical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             artificial sequence; vectors.
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                                                                                                                                                                                                                                                                                                Order or Technical 800-356-9526
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                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                  /note="T7 transcription initiation site"
                                                                                                                                                         /note="multiple cloning sites"
                                                                                                                             /note="T7 promoter"
/product="Beta-lactamase"
                                         /gene="bla"
                                 /c6don_start=1
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                                                                                                                                                                                                                                                                                                                                                           181 tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
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                                                                                                                                                                                                                 1891 TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGCAAAAT
361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                       2071 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGGAAAAGTGCCACCTGAC
                                                                                                                                           2011 CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT 2070
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/translation="MSIQHERVALIPFFAAFCLPVFAHPETLYKVKDAEDQLGRRIHYSONDLVE
IELDLNSGKILESERPEERFPMMSTEKVLLCGAVLSRIDAGQEQLGRRIHYSONDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFKELTAFLHNMGEADKVAGPL
DRWEFELNEAIPNOWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
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100.0%; Pred. No. 1.2e-274;
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1459 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1518
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                                                                    1399 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGGAAGCTAGAGTAAGT 1458
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                  61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
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                                                                                    1 cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
                                                                                                                                                   / Match 100.0%; '.Score 1001; DB 12; Length 2512; Local Similarity 100.0%; Pred. No. 1.2e-274; nes 1001; Conservative 0; Mismatches 0; Indels 0.
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Submitted (07-NOV-1997) Philippsen P., Applied Microbiology, University of Basel, Biozentrum, Klingelbergstr. 70, Basel,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wach,A., Brachat,A., Pohlmann,R. and Philippsen,P. New heterologous modules for classical or PCR-based disruptions in Saccharomyces cerevisiae Yeast 10 (13), 1793-1808 (1994)
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beta-lactamase; bla gene.
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                                                                                                                                                                                                                                                                                                                                                                           /product="beta-lactamase"
/protein_id="CAA05682.1"
/db_xref="GI:2623974"
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/transl_table=11 .
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                                                                                                pUC8 cloning vector
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                          Query Match
Best Local Similarity 100.0%; Pred. No. 1.
Matches 1001;
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ACCESSION VB0021
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#book Cloning Vectors, Elsvier 1985 and supplements
#comment vector I-A-iy-20
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mut 1408 A
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#journal Gene (1982) 19: 259-268
#comment. see also 'note added in proof'
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MARY pUC8 #length 2665
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/db_xref="taxon:32630"
680 c '670 g ' 661 t
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polylinker
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VecBase(3):pOM4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1150 GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                          421 ocacatagoagaactttaaaagtgotcatcattggaaaacgttcttcggggcgaaaactc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
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                                  550 GCGGGTGTTGGCGGGTGTCGGGGCTTGGCTTAACTATGCGGC
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                                                                                                                                                 841 tttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag 900
                                                                                                                                                                                       730
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                                                                                                                                                                                                                                                                                                      661 caatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgt 720
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                                                                                                                                                                                                                                                                                                                                                        gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
                                                                                                                                                                                                                                                                                                                                          GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTT
                                                 gcgggtgttggcgggtgtcggggctggcttaactatgcggc 1001
                                                                                                 acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 960
                                                                                                                                                                                      GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                                                                                  gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
                                                                                   ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA
                                                                                                                                     TTTCGTCTCGCGCGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCCGGAG
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SYNPUC9V/c LOCUS DEFINITION

pUC9 cloning vector

SYNPUC9V

2665 bp

DNA

circular

SYN

26-JUL-1993

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COMMENT
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VERSION
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         SUMMARY
                                                              SELECTION
                                                                     POLYLINKER HindIII-PstI-SalI-BamHI-SmaI-EcoR]
                                                                                                                FEATURE
                                                                                                                                                                                                                                                                                                                                                                     PARENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      These data and their annotation were supplied to GenBank by Will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                        pUC9 source
mut 1107 T C 3912 (c) pBR322
mut 1408 A G 3611 (c) pBR322
                  #resistance Ap*
#indicator Meta-galactosidase
                                                                                        931-1719 1-789 Ap-R; b-lactamase
                                                                                                                                                                                      Conflict
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269- 426
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2287/8 'AT' to 'TA' to match revised sequence of PBR322
The strand shown contains the beta-galactosidase mRNA sequence including the multiple cloning site of M13mp9.
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#journal Gene (1982) 19: 259-268
#comment see also 'note added in proof'
                                                                                                                                                                                                                                                                                            residue
1- 426
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VecBase(3):pIC19R
VecBase(3):pICEM19Hm, VecBase(3):pICEM19Hp,
VecBase(3):pICEM19Rm, VecBase(3):pICEM19Rp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1090 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGCGAAAACTC 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1150 GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
901 acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 960
                                          670 TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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                                                               841 tttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag 900
                                                                                                                        730 GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
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                                                                                                                                             781 gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc 840
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                                                                                                                                                                                                                                                                                                                                                                   910 GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTCCTTTTT 851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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pIC7 cloning vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obtained from VecBase 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   artificial sequence.
1 (bases 1 to 2668)
                                                                                                                                                            CROSSREFERENCE
                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *authors Marsh J.L., Erfle M., Wykes E.J.
#journal Gene (1984) 32: 481-485
#title
                                                                                                                                                                                                                           To produce greater versatility of insertional inactivation of beta-galactosidase activity for subcloning and sequencing, a chemically synthesized oligonucleotide, specifying nine restriction sites including BglII, Xhoi, NruI, ClaI, SacI and EcorV in various configurations with existing polylinkers, was created. These improved polylinkers were inserted into plasmids for routine cloning of ds-DNA and into chimeric phage/plasmids for biological production of ss-DNA. The most versatile polyrecognition pattern specifies 17 restriction sites in the beta-galactosidase alpha-complementing gene fragment. Clone beta-galactosidase alpha-complementing gene fragment. Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembled from pUC8 and GenBank:pIC7 by F. Pfeiffer COMMENT For construction of pTC7, a synthetic oligonucleotide has been used to replace the pUC8 polylinker and thus to construct a new cloning vector with a different polylinker. The other pIC-vectors are based on this new pIC7 polylinker, which was combined with the existing pUC9 and pUC19 polylinkers in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pIC19R: EcoRI- Poly (pIC7) -HindIII- Poly (pUC9) -EcoRI pIC19H: HindIII- Poly (pUC9) -EcoRI - Poly (pIC7) -HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pIC20R: EcoRI- Poly (pIC7) -HindIII- Poly(pUC19) -EcoRI pIC20H: HindIII- Poly(pUC19) -EcoRI - Poly (pIC7) -HindIII
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                                                                                                                                 #parent
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VecBase(3):pIC19H, VecBase(3):pIC19R,
VecBase(3):pIC20H, VecBase(3):pIC20R,
VecBase(3):pICEM19Hm, VecBase(3):pICEM19Hp,
                                                                                                      VecBase(3):pUC8, GenBank(50):pIC7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1513 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1453 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1394
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                                                                                                                                                                                               1033 TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCCACTCGTGCACCCAACTGA 974
                                                                                                                                                                                                                                                                  1093 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
                                                                                                                                                                                                                                                                                                                                           1153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 tyatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                                                                                          361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                         661 caatattattgaagcatttatcagggttattgtctcatgagcgggatacatatttgaatgt 720
                                                                                                                                                                                                                                  481
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                                                                                                                                                                                                                                                                                       | ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
                                                                                                                                                                                                                                                                                                                                         GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
                                                    gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
                                                                                                                                                                                                                             tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
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_YLINKER ECORI-ClaI-ECORY-XbaI-BglII-XhOI-SacI-NruI-HindIII
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1- 235
230- 268
263-2668
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MARY pIC7 #length 2668 #
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/db_xref="taxon:32630"
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260-2665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1001; DB 12; Length 2668; Pred. No. 1.2e-274;
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polylinker of pIC7
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961 gcgggtgttggcgggtgtcgg@gctggcttaactatgcggc 1001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic construct DNA.
Synthetic construct
artificial sequence.
1 (bases 1 to 2674)
Gilbert, W.
                                                                                                                                                  CROSSREFERENCE #complement :
                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE pUC7 - Cloning vector
DATE 17-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. pUC7
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION VB0020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning vector
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L08958.1 GI:310823
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           VecBase(3):pUC8, VecBase(3):pUC9, VecBase(3):pUR222 PARENT
Features of pUC7 (2674 bp)
                                                         #parent
VecBase(3):pBR322, VecBase(3):M13mp7,
GenRank(50):EcoLac, VecSource(3):bGa17
                                                                                                                                                                                                  Assembled from pUC19 and M13mp7 by F. Pfeiffer, MPI, Martinsried Revised 16-DEC-1986 by F. Pfeiffer:
2296/7 'AT' to 'TA' to match revised sequence of PBR322
The strand shown contains the beta-galactosidase mRNA sequence including the multiple cloning site of M13mp7.
                                                                                                                                                                                                                                                                                                                                                                                                            #authors Vieira J., Messing J.
#journal Gene (1982) 19: 259-268
#Comment see walso 'note added in proof'
                                                 offspring#
                                                                                                                                                                                                                                                                                                                         #comment vector I-A-iv-20
                                                                                                                                                                                                                                                                                                                                       #authors Pouwels P.H., Enger-Valk B.E.,
                                                                                                                                                                                                                                                                                                                                                                                    #number 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #number 1
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                                                                                                                            VecBase(3):pUC7c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 1001;
                                                                                                     1039 TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA
                                                                                                                                                           1099 CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGCGAAAACTC 1040
                                                                                                                                                                                                              1159 GANTAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
                                                                                                                                                                                                                                                                  421 ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
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                                                                                                                      481 tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 540
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tgatccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                                                                                                                                                                                                     AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT
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#Indicator beta-galactosidase
#MARY pUC7 #Length 2674 /
Location/Qualifiers
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mut 1116 T C 3912 (c) pBR322
mut 1417 A G 3611 (c) pBR322
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1- 229
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                       CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1346
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pUC13 DNA sequence.
A02712
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1 (bases 1 to 2680)
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                                                                                                                                                                                                                                                                     h 100.0%;
Similarity 100.0%;
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683 c 676 g
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                                                                                                                                                Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
                                                                                                                                                                                              Gilbert, W
                                                                                                                                                                                                                                        synthetic construct
                                                                                                                                                                                                                                                      Synthetic construct DNA.
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                                                                            TITLE pUC12 - Cloning vector DATE 17-SEP-1986
                                                                                                                     Cloning vector
                                                                                                                                    Gilbert under the auspices
                                                                                                                                                                               Obtained from VecBase 3.0
                                                                                                                                                                                                                           artificial sequence
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                                          ACCESSION VB0023
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#number
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                                                                                                                                                                                                                                                                                                                   cloning
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                                                          tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                                                   cgctcgtcgtttggtattggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                                                                                                                                          AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1406
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agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact
                                    TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1286
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WARY pUC12 ,#length 2680
Location/Qualifiers
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    pUC12. source
    mut 1122 T C 3912 (c) pBR322
    mut 1423 A G 3611 (c) pBR322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #authors Pouwels P.H., Enger-Velk B.E., Brammar W.J.
#book Cloning Vectors, Elsvier 1985 and supplements
#comment vector I-A-IV-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #authors Vieira J., Messing J.
#journal Gene (1982) 19: 259-268
#comment see 'note added in proof'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #offspring
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                                                                    Gene 19 (
83106470
                                                                                                                       artificial sequence; vectors 1 (bases 1 to 2680) Vieira, J. and Messing, J.
Unpublished
                          Gilbert, W.
                                                                                              The pUC plasmids, an M13mp7-derived system for insertion mutagenesis and sequencing with synthetic universal prim
                                                                                                                                                                       Cloning vector pUC13
Cloning vector pUC13
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Cloning vector pUC13,
            Obtained
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. pUC13 Cloning vector
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mut 1122 T C 3912 (c) pBR322
mut 1423 A G 3611 (c) pBR322
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#journal Gene (1982) 19: 259-268
#comment see 'note added in proof'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #parent
VecBase(9):pUC9, VecBase(3):M13mp11, VecSource(3):bGal13
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MARY pUC13 #length 2680
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679-2680
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VecBase(3):pSP65, VecBase(3):pGEM2, VecBase(3):pT713 PARENT
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233. .283
                                                      /note="pBR322"
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                                          /note="Ap-R"
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SUMMARIES

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Nucleotide sequenc	Plasmid protos enc Plasmid pGM678 con Plasmid pGM679 con	DNA sequence of the Nucleotide sequence	Plasmid pSP72. Es Plasmid vector pUC Tn7 target plasmid	Description

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AAX77614 AAX79291 AAZ22045 AAC22045 AAC82936 AAC82936 AAD09269	AAV39243 AAV39243 AAZ21997 AAF55224 AAV12068 AAX77617	AAZ39628 AAF55225 AAV12067 AAT78802	AAF26094 AAF26094 AAC55541 AAQ04010 AAF59062	AAT69188 AAT69189 AAA51634 AAAF26077 AAT58319	AAZ21996 AAF26078 AAX61041 AAV00679 AAQ70942	AAD04947 AAV39242 AAT78801
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ALIGNMENTS

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AAA74638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                  Plasmid pSP72; NSE-p25 transgene; p25; cdk5 activator; neuron specific enolase; NSE; promoter; neurodegenerative disease; nativatoral sclerosis; Alzheimer's disease; parkinson's disease; amyeLolateral sclerosis; Huntington's disease; traumatic brain hojury; stroke; transgenic animal; Huntington's disease; traumatic brain hojury; stroke; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                05-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                           AAA74638;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA74638 standard;
                                                                                                                                                                                                                                                               spinocerebellar degeneration; tau hyperphosphorylation;
                                                                                                                                                                                                                                                                                                                                                   Plasmid pSP72.
New recombinant DNA molecule comprising gene encoding p25, useful for producing transgenic animal to serve as model for % \left( 1\right) =200
                                                                                                                           03-FEB-1999;
                                                                                                                                                                                   09-AUG-2000.
                                                                                                                                                                                                             EP1026251-A2
                                                                                                                                                                                                                                        Escherichia coli.
                                            WPI; 2000-507252/46.
                                                                   Ahlijanian MK, Mcneish JD;
                                                                                               (PFIZ ) PFIZER PROD INC
                                                                                                                                                     02-FEB-2000; 2000EP-0300797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        2462 BP.
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The present sequence is the commercially available plasmid pSP72. The CS SV40 polyadenylation sequence, the rat neuron specific enclase (NSE) promoter and the human cDNA for p25 were cloned into plasmid pSP72 to GC generate the NSE-p25 transgene. This was used in the production of CC cdx5. Overexpression of p25 is sufficient to produce hyperphosphorylation CC of tau, which is seen in the neurofibrillary tangles associated with CC Alzheimer's disease. The transgenic animals are useful as in vivo systems CC for screening potential therapeutic compounds for their ability to CC inhibit or prevent the production of hyperphosphorylated tau and CC associated neuronal death. The transgenic animals are suitable for use as Gisease models of neurodegenerative diseases and tau-related pathologies, CC such as Alzheimer's disease, Parkinson's disease, amyelolateral CC sclerosis, Huntington's disease, Stroke, traumatic brain injury, CC spinocerebellar degeneration. They are also useful as models of cdk5/p25 and tau biochemistry, and to establish the role of the human p25 in the formation of hyperphosphorylated tau in neurodegenerative conditions.
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                                         tetteageatettttaattteaceagegitteetgggtgageaaaaaeaggaaggeaaaat
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1001; No. 3

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                                      its polymerizate, where the peptide (I) has a formula of: alpha1-alpha2-alpha3-alpha4-alpha5-alpha6-alpha7 where alpha1 to alpha7 = amino acid sequence selected from amino acid sequences ranging from 11-19 amino acids derived from T cell epitopes derived from cedar (Japanese cedar - Cryptomeria Japonica) pollen allergens. The peptide can be used in an antisugipollinosis agent AAF5911 to AAF59062 and AAB69194 to AAB69121 represent sequences used
Sequence 2686 BP; 661 A; 685 C;
                                 'n
                                                                                                                                                   The present invention describes a peptide, its complex,
                                                                                                                                                                                                                                                WPI; 2001-185061/19.
                                                                                                                                                                                    Example 11;
                                                                                                                                                                                                                 Novel peptide and its use
                                                                                                                                                                                                                                                                                                                         15-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T cell epitope; antisugipollinosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid vector pUC18M5 nucleotide sequence SEQ ID NO:70.
                                                                                                                                                                                                                                                                           (HAYB ) HAYASHIBARA SEIBUTSU (SANY ) SANKYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                        15-MAR-2000; 2000JP-0071710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Japanese cedar; Cryptomeria japonica; cedar pollen allergen;
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                            exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA;
                                                                                                                                                                                Page 61-63; 75pp; Japanese.
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AAV32980 standard; DNA; 3190 BP.

Tn7 target plasmid sequence 17-NOV-1998 (first entry)

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           gcgggtgttggcgggtgtcgggggctggcttaactatgcggc.1001
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                                                            acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 960
                                                                                                TTTCGTCTCGCGCGTTTCGGTGATGAĊGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transposon(s) encoding mutant ATP using proteins for insertion which is efficient and random, with reduced site specificity; for DNA sequencing and altering gene expression
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                                       gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga
                                                                                                                                                                    cgctcgtcgtttggtatggcttcattcagctccggttccccaacgatcaaggcgagttaca 180
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                        (HEAL-) HEALTH RES INC. .
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      PinPoint vector; fusion protein antigen; membrane antigen; syphilis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ99245 standard; DNA; 3331 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a PinPoint expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2000 (first entry)
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                        the course of the invention. The specification describes a method for detecting antibodies against Treponema pallidum. The antibodies are detected in a sample by reaction with a fusion protein antigen, present in the mixture in limiting concentration. The fusion protein antigen comprises a Treponema pallidum membrane antigen. The method is used for diagnosis of syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                           EP985931-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                     Treponema pallidum.
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                                                                                                                                                                      Immunoassay for anti-Treponema pallidum antibodies, used for diagnosis of syphilis using a fusion protein of membrane antigen with peptide sequence that can be biotinylated in vivo
                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                      04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                 12-AUG-1999;
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                                                                                                                                           Disclosure; Page 8-9; 16pp; English.
                                                                                                                                                                                                                                                             Mullenix MC,
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                                                                                                               present sequence represents the PinPoint vector, which is used in
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Sequence 3331 BP;

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                                               gtotaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
                                                                                                                                                                                                  ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGGAAAAGTGCCACCTGAC
                                                                                                                                                                                                              atttagaaaaataaacaaataqqqqttccgcgcacatttccccgaaaaqtgccacctgac
                                                                                                                                                                                                                                                    CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT
            gcgggtgttggcgggtgtcggggctggcttaactatgcggc
                                                                                                TTTCGTCTCGCGCGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
                                                                                                               tttcgtctcgcgcgttttcggtgatgacggtgaaaacctctgacacatgcagctcccggag
GCGGGTGTTGGCGGGTGTCGGGGCTTGGCTTAACTATGCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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AAQ04655/c
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        1948
                                                                                                                                                                                                               2188 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2129
                                                                                                                                                                      2128
                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pBT111 encoding the kappa chain and plasmid AAP10169 encoding the Fd chain of antibody MAK33 were used to transform E. coli DSM 3689 and the resulting cells grown to form inclusion bodies. After the final renaturation step an 18% yield of biologically-active protein was
                                                                                                                                                                                                                                                                                                                                            Sequence 3343 BP; 815 A; 871 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; p; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Activated antibody prodn. from recombinant procaryotic cells by solubilisation under reducing conditions, then oxidative renaturation, carried out at low protein concn.
                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                          see also AAQ04654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-156813/21
              241 agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-OCT-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody MAK33; Fd chain; plasmid p10169; activated antibody prodn.; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid p10169 encoding antibody MAK33 Fd chain
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                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                               1 cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT 1889
                                                                tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                                                     cgctcgtcgtttggtattggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                  TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA 1949
                                                                                                                                                          AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA
                                                                                                                                                                           agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= Fd chain of MAK33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 240..917
                                                                                                                                                                                                                                                                                    100.0%; Score 1001; DB 11; 100.0%; Pred. No. 3.8e-263;
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                                                                                                                                                                                                                                                                                                DB 11; Length 3343;
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                                                                                                                                         Uridine phosphorylase; udp; purine nucleoside phosphorylase; PNP; deo Genetically modified organism; catalyst; transglycosylation; nucleoside analogue; alpha-pentose-1-phosphate sugar; phosphorolysis; anti-viral; anti-tumour; mesophilic bacterium; ss.
                                                          misc_RNA
                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                     Plasmid pGM678 containing E. coli deoD gene.
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                                                                                                      Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC
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              /label= pUC18_sequence 216..952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC catalysts of transglycosylation reactions between a donor nucleoside and cc an acceptor base, for preparing nucleoside analogues containing cone or more nitrogen atoms, for preparing nucleoside analogues containing cone or more nitrogen atoms, for preparing alpha-pentose-1-phosphate cone or more nitrogen atoms, for preparing alpha-pentose-1-phosphate condified nucleosides and notified nucleosides and services (all claimed). The modified or natural concessides are used directly or as intermediates in the preparation of concleosides are used directly or as intermediates in the preparation of concessides are used directly or as intermediates in the preparation of concessides are used directly or as intermediates in the preparation of congraw with anti-viral and anti-tumour activity and for preparing configuration of the calls are produced using recombinant plasmid expression vectors comprising at least one gene sequence of a mesophilic bacterium coding comprising at least one gene sequence of a mesophilic bacterium coding comprising at least one gene sequence of a mesophilic bacterium coding comprising at least one genes are used. Recombinant strains produced consing the vectors express polypeptides with enzyme Upp and PNP activity in large amounts, e.g. 340-1040 times higher Udp and PNP activity and 120-200 contains higher pNP activity than non-transformed corresponding wild type
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        Matches 1001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Host cells genetically modified to express uridine phosphorylase (UdP) and purine nucleoside phosphorylase (PNP) or their corresponding crude or purified extracts, either separately or in combination are used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant expression vectors used to transform cells for the production of e.g. nucleosides encode uridine phosphorylase and
                                                                                                                                                                                                                                           2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3383 BP; 826 A; 868 C; 855 G; 834 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 47-48; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NORP-) NORPHARMA SPA
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                                                                                                                                                                                                                                                                                                         CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2169
                                                                                                                                                                                                                                                                                                                                           cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
                                                                                                                                                                              cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                                                                                                                                                                                           AGTTCGCCAGTTAATAGTTTGCCCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA
                                                                                                                                                          CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA
agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact
                                                                        TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
                                                                                                 tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga
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                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1001; DB 21; 100.0%; Pred. No. 3.8e-263; Live 0; Mismatches 0;
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                                                                                                             Uridine phosphorylase; udp; purine nucleoside phosphorylase; PNP; deoD; Genetically modified organism; catalyst; transglycosylation; nucleoside analogue; alpha-pentose-1-phosphate sugar; phosphorolysis; anti-viral; anti-tumour; mesophilic bacterium; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1448
CDS
                                                                                                                                                                                                                                                           AAA51630 standard; DNA; 3444 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481
                                    misc_RNA
                                                                         Synthetic
                                                                                                                                                                              Plasmid pGM679 containing E. coli udp gene.
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                                                                                        Escherichia
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                                                                                                                                                                                                                                                                                                                           GCGGGTGTTGGCGGGTGTCGGGGGCTTAACTATGCGGC 1228
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                                                                                       coli.
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/label= pUC18_sequence
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                                                 Location/Qualifiers
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CC and purine nucleoside phosphorylase (PNP) or their corresponding crude or
CC purified extracts, either separately or in combination are used as
CC catalysts of transglycosylation reactions between a donor nucleoside and
CC an acceptor base, forpreparing nucleoside analogues containing
CC one or more nitrogen atoms, for preparing alpha-pentose-1-phosphate
CC sugars by phosphorolysis reactions and for producing nucleosides and
CC modified nucleoside analogues (all claimed). The modified or natural
CC nucleosides are used directly or as intermediates in the preparation of
CC drugs with anti-viral and anti-tumour activity and for preparing
CC oligonucleotides for therapeutic or diagnostic use. The recombinant host
CC comprising at least one gene sequence of a mesophilic bacterium coding
CC comprising at least one gene sequence of a mesophilic bacterium coding
CC comprising at least one gene sequence of a mesophilic bacterium coding
CC comprising the vectors express polypeptides with enzyme UNP activity and at
CC least one gene sequence coding for antibiotic resistance. In particular,
CC the E. coli udp and deoD genes are used. Recombinant strains produced
CC using the vectors express polypeptides with enzyme UNP activity
in large amounts, e.g.. 340-1040 times higher UNP activity and 120-200
CC times higher NNP activity than non-transformed corresponding wild type
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                            2109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant expression vectors used to production of e.g. nucleosides encode u purine nucleoside phosphory ase
                         241
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agtaagttggccgcagtgttatcactcatggttatggcagcactgcataattctcttact
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                                                                         tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga
                                                        TGATCCCCCATGTTGTGCAAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
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                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1001; DB 21; Length 100.0%; Pred. No. 3.8e-263;
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                                                    WO9713852-A1
                                                                                                                     transgenic; mouse; CD4; antibody; autoimmune;
transplant rejection; immunoglobulin; ss.
                                                                                                                                                                         Kappa light chain plasmid pLC6G5
                                                                                                                                                                                                         23-JAN-1998
                                                                                                                                                                                                                                                              AAT78825 standard;
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                                                                                                                                                                                                                                                                                                                                                                                Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; CD4 binding; autoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
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                                                                      Hybridoma producing antibody specific for interleukin-8 - prevent efflux of neutrophils from vasculature, and treat
                                                                                                                                                                                                                                      01-DEC-1997;
                                                                                                                                                                                                                                                                                                  WO9824884-A1
                                                                                                                                                                                                                                                                                                                                                                      cystic fibrosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pLC6G5 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-DEC-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV39266 standard;
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                                                                                                                     WPI; 1998-333306/29.
                                                                                                                                                                                                         02-DEC-1996;
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                            Example 42; Pages 317-319; 452pp; English.
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The present sequence represents a plasmid, pLC6G5,

which contains

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initiation sites are incorporated and HindII sites were engineered upstream of the translation initiation sites. The plasmid is used in the construction of minigenes for expression of IgGkappa anti-CD4 antibodies, in the transgenic mouse of the invention. The specification describes transgenic non-human animals, especially a mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals have human heavy and light chain transgenes. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-J) recombination. The transgenes
                                injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The anti-IL-8 antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                       include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and on constant region gene segment. The gene segments are heterologous to the transgenic animal. The antibody can be used to prevent efflux of neutrophils from vasculature. It can also be used to treat reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic kappa light chain sequence (created using oligonucleotide AAV39244-65). This synthetic sequence differs from natural sequences in that strings of repeated oligonucleotides are interrupted (to facilitate oligonucleotide synthesis and PCR amplification), optimal translation
asthma) and cystic fibrosis.
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947 A; 1015 C; 912 G; 945 T; 0 other;

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tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaacaggaaggcaaaat
                                                                                                                                       CCacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
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                                                   tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga 1695
                                                                  tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactga
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Pred. No. 3.9e-263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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producing a heterologous antibody. The antibodies are isolated form hybridoma, comprising B cells, that is obtained from a transgenic me having a genome comprising a human heavy chain transgene and a human light chain transgene. The B cells are fused to immortalized cells The specification describes transgenic animals that are capable

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RESULT 1
AAZ22020
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                                                                                                                  antibodies
                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic animal; heterologous antibody; hybridoma; B cell; transgenic mouse; human heavy chain transgene; digoxin; human light chain transgene; immortalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1996
                                                                                     Example 42;
                                                                                                                               Novel transgenic
                                                                                                                                                              WPI; 1999-551219/46
                                                                                                                                                                                                                       (GENP-) GENPHARM INT INC
                                                                                                                                                                                                                                                    13-MAR-1998;
                                                                                                                                                                                                                                                                                                              16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                 transplant rejection; blood disorder; coagulation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1936
                                                                                                                                                                                         Lonberg N,
                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of plasmid pLC6G5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 3819
                                                                                  Page 318-320; 484pp; English.
                                                                                                                                                                                         Fishwild DM,
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                                                                                                                               non-human animals used to
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                                                                                                                               produce heterologous
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Matches 1001;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention can be used to treat human diseases, e.g. autoimmune diseases, cancer, infectious disease, transplant rejection, blo disorders such as coagulation disorders and other diseases. The present sequence is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    suitable for generating a hybridoma, which produces a detectable amount of an immunoglobulin that specifically binds digoxin or Shinga-like toxin. B cells from transgenic animals can be used to generate hybridomas expressing monoclonal high affinity human sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1576
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gtctaagaaaccattattatçatgacattaacctataaaaataggcgtatcacgaggccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         947 A; 1015 C;
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                                                                                        The present invention relates to a conditional gene trapping construct capable of causing conditional mutations in genes. The gene trapping construct comprises two functional DNA segments, each being flanked by two recombinase recognition sequences (RRSs) specific to site specific recombinase which is capable of unidirectional inversion of double standard DNA segment. One of the DNA segment (disruption cassette) is inserted in antisense orientation relative to the transcriptional orientation of the gene to be trapped. The other DNA segment (selection cassette) is inserted in sense direction relative to the transcriptional orientation of the gene to be trapped. The coll comprising the gene trapping construct is useful for the identification and/or isolation of genes. The transgenic organism comprising the gene trapping construct is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD04947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric -
                                         useful to study gene function at various developmental stages. The gene trapping construct is useful for mutationally inactivating all cellular genes. The present sequence is pRK50 vector, which is used to test Cre
                                                                                                                                                                                                                                                                                                                                                    New gene trapping construct capable of causing conditional mutations genes, comprises functional DNA segment inserted in sense or antisens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              selection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene trapping construct; conditional mutation; unidirectional inversion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pRK50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FRAN-)
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27-OCT-1999;
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                               recombinase mediated inversion, which is related to the
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Unidentified.
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GCGGGTGTTGGCGGGTGTCGGGGTTGGCTTAACTATGCGGC 1435
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RESULT 13
AAV39242
 The present sequence represents the kappa light chain plasmid, pCK7-96, which includes the kappa constant region and polyadenylation site. The CC plasmid is used in the construction of minigenes for expression of CC Igdkappa anti-CD4 antibodies, in the transgenic mouse of the invention. CC The specification describes transgenic non-human animals, especially a cc mouse, which are capable of producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals compared to the constant reasonable of functionally rearranging a heterologous diversity. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a cc variable-diversity-junction (V-D-J) recombination. The transgenes include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and one constant cc animal. The antibody can be used to prevent efflux of neutrophils from cv asculature. It can also be used to treat reperfusion injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The canimal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used for the treatment of vasculitis, septic shock, allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isotype switching; neutrophil efflux; reperfusion injury; CD4 binding; autoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybridoma producing antibody specific for interleukin-8 - prevent efflux of neutrophils from vasculature, and treat
Sequence
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 981 A; 1013 C; 921 G;
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Local Similarity

100.0%; ilarity 100.0%; Conservative

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Score 1001; DB 1 Pred. No. 4e-263; Mismatches 0

DB 19;

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Indels

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RESULT AAT78801

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AAT78801 standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel composition has been developed which comprises an immunoglobulin (19) having an affinity constant (Ka) of at least 2 multiply 1000000000 M-1 for binding to a predetermined human antigen. The present sequence represents the kappa light chain plasmid pCK7-96 which includes the kappa constant region and polyadenylation site. Anti-CD4 antibodies may be used in therapeutic and diagnostic applications, especially for the treatment of human diseases. These antibodies reduce activity of CD4 cells and reduce undesirable autoimmune reactions, inflammatory response and transplant rejection. Transgenic animals are capable of producing heterologous antibodies of multiple isotypes by undergoing isotype switching. These animals produce a first 1g type that is necessary for antigen-stimulated B-cell maturation and can switch to encode and produce one or more subsequent heterologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment of auto-immune disease etc.
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Pred. No. 4e-263;
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                                                                                                                                                 Transgenic animal; heterologous antibody; hybridoma; B cell; transgenic mouse; human heavy chain transgene; digoxih; human light chain transgene; importalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                          2116
13-MAR-1998;
                           12-MAR-1999;
                                                                                W09945962-A1
                                                                                                                                     transplant
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                                                                                                                                                                                                                      sequence of plasmid pCK7-96
                                                                                                                                    rejection; blood disorder; coagulation disorder; ss
98US-0042353
                           99WO-US05535
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Best Local
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1156
                                                                                                                                                                                 diseases, cancer, infectious disease, transplant rejection, disorders such as coagulation disorders and other diseases. present sequence is used in the course of the invention.
                                                                                                                                                   Sequence 3881 BP;
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ilarity 100.0%;
Conservative (
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Pred. No. 4e-263;
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                                                                Mismatches
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gcgggtgttggcgggtgtcgggcttaactatgcggc 2156	gcgggtgttggcgggtgtcgggcttgactatgcggc 1001	acggtcacagcttgtctgtaagcggatgccgggagcagacaagcccgtcagggcgcgtca 2115	acggtcacagcttgtctgtaagcggatgccgggaggcaagccaggccgtcagggcgcgtca 960	ttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag 2055	tttcgtctcgcgcgttttcggtgatgacggtgaaaacctctgacacatgcagctcccggag 900	gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc 1995	gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc 840	atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac 1935	atttagaaaaataaaccaaataggggttccgcgcacatttccccgaaaagtgccacctgac 780	caatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgt 1875	caatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgt 720	gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 1815	gccgcaaaaaagggaataagggcgaćacggaaatgttgaatactcatactctttccttttt 660

Search completed: January 8, 2002, 17:27:47 Job time: 12647 sec

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OM nucleic - nucleic search, using sw model
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Maximum DB
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seq length: 2000000000
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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             3343 6
3819 4
3875 4
38775 4
38776 4
3878 6
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3881 4
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US-09-039-641-27
US-09-039-762A-21
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US-09-039-762A-24
US-08-758-430-3
US-08-09-039-762A-24
US-08-09-039-762A-24
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US-08-371-320-1
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US-09-039-762A-21
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US-09-039-982A-21
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1279.226 Million cell updates/sec
                                                                                                         Patent No. 5453363
Sequence 243, App
Sequence 21, Appl
Sequence 21, Appl
Sequence 27, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 24, Appl
Sequence 54, Appl
Sequence 3, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 15, Appl
Sequence 218, App
Sequence 218, App
Sequence 418, App
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Sequence 1, Appli
Setent No. 5453363
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PCT-US94-00658-1	US-08-659-206A-4	US-08-893-327-19	US-08-893-327-17	US-08-893-327-15	US-09-011-745-6	US-09-011-745-5	US-09-011-745-8	US-09-175-690A-1	US-08-793-610-4	US-08-793-610-1	US-08-793-610-2	US-08-793-610-3	US-09-498-599-5	US-08-801-344-5	US-08-929-967-16	US-08-789-333F-58	US-08-758-417A-268
Sequence 1, Appl1	Sequence 4, Appli	Sequence 19, Appl	17,	Sequence 15, Appl	Sequence 6, Appli	Sequence 5, Appli	Œ	Sequence 1, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 3, Appli	Sequence 5, Appli	ı v	Sequence 16, App1	Sequence 58, Appr	268,

ALIGNMENTS

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RESULT 1
US-07-415-307A-1
US-07-415-307A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP89/0026
FILING DATE: 12-Jan-1989
APPLICATION NUMBER: DE 38 00 642.1
FILING DATE: 12-Jan-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5344757man D.
REGISTRATION NUMBER: 30,946
REGISTRATION NUMBER: BOER 798
TELECOMMUNICATION NECOMMETTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kessler, Christoph
APPLICANT: Mattes, Ralf
TITLE OF INVENTION: Process for the Detection of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Holtke, Hans Joachim
APPLICANT: Seibl, Rudolf
APPLICANT: Schnitz, Gudrun
APPLICANT: Scholer, Hans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC/DO SOFTWARE: WORDERFECT CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 212-688-9200
                                           TENGTH: 310+ - Sing
                                                                                                                        TELEPHONE: 212-00-
TELEPHONE: 212-838-3884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US
FILING DATE: 19900109
                                         STRANDEDNESS:
                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10022
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                                                                               3104 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diskette, 5.25 inch,
                                       single
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Matches 1001; Query Match

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           GCGGGTGTTGGCGGGTGTCGGGCTTGGCTTAACTATGCGGC
                                                                                                                                                                                                                                                                              GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
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                                                                                                 ACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA
                                                                                                                                                                                     TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA
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                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 1001; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 07/415,307
FILING DATE: 09-Tan-1990
APPLICATION NUMBER: PCT/EP89/0026
FILING DATE: 12-Tan-1989
APPLICATION NUMBER: DE 38 00 642.1
FILING DATE: 12-Tan-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
APPLICATION NUMBER: DE 38 13 278.8
FILING DATE: 20-Apr-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Holtke, Hans Joachim
APPLICANT: Scibl, Rudolf
APPLICANT: Scholer, Gladrun
APPLICANT: Scholer, Hans
APPLICANT: Kessler, Christoph
APPLICANT: Mattes, Ralf
TITLE OF INVENTION: Process for
                                                                                                                                                                                                                      NAME: Hanson, No. 5702888man D. REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 7
TELECOMMUNICATION INFORMATION:
                                                                                                                                  1609 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYDE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC/DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/371,320
FILING DATE: 11-JAN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                       61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 805 Third Avenue CITY: New York City STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 10022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
tgatcccccatgttgtgcaaaaaagcggttagctccttcggtcctccgatcgttgtcaga 240
                                                                 cgctcgtcgtttggtattggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                            CGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACA 1728
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                                                                                                                                                           Patent No. 5453363
APPLICATION NUMBER: US/08/20
FILING DATE: 02-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 942,370
FILING DATE: 09-SEP-1992
APPLICATION NUMBER: 498,500
FILING DATE: 23-MAR-1990
APPLICATION NUMBER: 76,207
FILING DATE: 23-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1849
                                                                                                  APPLICANT: RUDOLPH, RAINER; FISCHER, STEE
TITLE OF INVENTION: PROCESS FOR THE ACTI
AFTER GENETIC EXPRESSION IN PROKARYOTES
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
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ACTIVATION OF T-PA OR
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Local Similarity 100.0%;
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                                                     tttcgtctcgcgcgtttcggtgatgacggtgaaaacctctgacacatgcagctcccggag
                                                                                                                               ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC
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                                            TTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAG
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Pred. No. 2.2e-301;
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                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 08/UD3/131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
                                                                                                                                                                                                             FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 18-NOV-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
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FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                             PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                     APPLICATION NUMBER: US OF THE DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/161,739 FILING DATE: 03-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 16-DE
                                                                                                                                                                         APPLICATION NUMBER: US 0:
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 22-JUI
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/209,741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 13-MA
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER: US 08/155,301
18-NOV-1993
                                                                                                                   10-OCT-1995
                                                                                                                                                                                                                                                                                           10-DEC-1993
JMBER: WO PCT/US96/16433
10-OCT-1996
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Best Local Similarity
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APPLICATION NUMBER: U:
FILING DATE: 02-DC-1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W
                                                 1756 GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTT 1815
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                                                                                                                        1696 TCTTCAGCATCTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT
                                                                                                                                                                                              1636 TCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
661 caatattattgaagcatttatcagggttattgtctcatgagcggatacatatttgaatgt 720
                                                                                                                                         541 tcttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaat 600
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              481 tcaaggatcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaaactga 540
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ADDRESSEE: Townsend and Townsend and Crew LLP
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MEDIUM TYPE: Floppy disk
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                                FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/758,417A FILING DATE: 02-Dec-1996
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STATE: California
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                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/728,463 FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/209,741 FILING DATE: 09-MAR-1994
                                                                                                                                                                        APPLICATION NUMBER: US 08/155,301 FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/544,404
REGISTRATION NUMBER: 41,303
                    NAME: Serafini,
                                                                                                                FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
                                                                                                                                                     APPLICATION NUMBER: US 08/096,762
                                                                                                                                                                                                                 FILING DATE: 03-DEC-1993
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TOPOLOGY: linear;
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID
US-08-758-417A-243
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 243:
SEQUENCE CHARACTERISTICS:
LENGTH: 3819 base pairs
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                                                                       atttagaaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac 780
                                                                                                                                                                                                GCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTTTTT
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STRANDEDNESS: single
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Pred. No. 2.3e-301;
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Best Local Similarity
                                                                                                                                          Matches 1001;
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                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-MAR-1998 (CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OLSON, ARNE M., 30,203
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSR14710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 3875 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
     2431 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 2372
                                                                     2491 CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2432
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                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: 9
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TITLE OF INVENTION: ANTIGEN PRESENTING
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                      61 agttcgccagttaatagtttgcgcaacgttgttgccattgctacaggcatcgtggtgtca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            841 tttcgtctcgcgcgttttcggtgatgàcggtgaaaacctctgacacatgcagctcccggag 900
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                                                                                     1 cctgcaactttatccgcctccatccagtctattaattgttgccgggaagctagagtaagt 60
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                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
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20 No. 6225042th Wacker Drive,
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Brunmark, Anders
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Pred. No. 2.4e-301;
Mismatches 0;
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                                                              Sequence 21, Application of the control of S51627 GENERAL INFORMATION:
APPLICANT: Ca1, Ze1
APPLICANT: Sprent,
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     OF INVENTION:
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                                                                                                                                  Application US/09039641
          Sprent, Jonathan Brunmark, Anders Jackson, Michael Peterson, Per A
                                                                                   Zeling
 ANTIGEN
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SYSTEM AND

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CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES:

ACTIVATION OF T-CELLS

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ATTORNEY/AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELECHEORE: (312) 580-1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 21:
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MEDIUM TYPE: Flopp# disk
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LENGTH: 3875 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                           2311 TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 8-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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                ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcgggggcgaaaactc 480
                                                               gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga 360
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CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGGGAAAACTC 2012
                                                                                                                                     GTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGA 2132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Cai, Zeling
APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 21, Application US/09039762A Patent No. 6255073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1651 TTTCGTCTCGCGCGTTTCGGTGATGACCGTGAAAACCTCTGACACATGCACCTCCCGGAG
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 REFERENCE/DOCKET NUMBER: TS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEPAX: (312) 580-1189
                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                             ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,
                                                                                                                                                       SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             STREET: 20 NO. CITY: Chicago
                                                                                                         FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                     ZIP: 60606
                                                                                                                                                                                                                                                                 COUNTRY:
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TELEPHONE:
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20 No. 6255073th Wacker Drive, 36th Floor
                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                      PatentIn Release #1.0,
                                                                                                                     IUMBER: US/09/039,762A
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                                                 TSRI 471.0 DIV.2
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INFORMATION FOR SEQ ID NO:

21:

SEQUENCE CHARACTERISTICS: LENGTH: 3875 base pairs

TYPE: nucleic acid STRANDEDNESS: double

MOLECULE TYPE:

TOPOLOGY:

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                                                                    GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                                                             ATTTAGAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC 1712
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Pred. No. 2
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2.4e-301;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: Olson, Arne M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                 MOLECULE
HYPOTHETICAL: NO
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LENGTH: 3878 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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APPLICANT: Sprent, Jonathan
APPLICANT: Brunmark, Anders
121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca
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APPLICANT: Peterson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA
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(312) 58
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Peterson, Per A
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   GENERAL INFORMATION:
APPLICANT: Cai, Zeling APPLICANT: Sprent, Jonathay APPLICANT: Brunmark, Anders APPLICANT: Brunmark, Anders APPLICANT: Holden, Michael, APPLICANT: Heterson, Michael, APPLICANT: Heterson, Per A APPLICANT: Heterson, Per A TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND MET TITLE OF INVENTION: ACTIVATION OF T-CELLS NUMBER OF SEQUENCES: 45
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                                                                                                                                                                   Sequence 27, Application US/09039641 Patent No. 6251627
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CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 27:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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LENGTH: 3878 base pairs
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
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STRANDEDNESS: double
TOPOLOGY: linear
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361
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                                                                                   ccacatagcagaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactc 480
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                                                                   CCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGCGAAAACTC
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20 No. 6251627th Wacker Drive, Suite 3000
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TYPE:

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US-09-039-762A-27/c

: Sequence 27, Application US/09039762A

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APPLICANT: Sprent, Jonathan
APPLICANT: Sprent, Jonathan
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A.
                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                       SEQUENCE CHARACTERISTICS:
                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: OLSON, Arne M.
REGISTRATION NUMBER: 30,203
                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION MATA:
APPLICATION NUMBER: US/09/039,762A
FILING DATE: 16-MAR-1998
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIGEN PRESENTING SYSTEM AND METHODS TITLE OF INVENTION: FOR ACTIVATION OF T-CELLS NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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N: 435
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1714 GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCC
                                                                                                                                          1774 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTGAC
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HYPOTHETICAL: NO
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                                                                                          781 gtctaagaaaccattattatcatgacattaacctataaaaataggcgtatcacgaggccc
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APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-9991
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/853,408
FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                          FILING DATE: 18-NOV-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC.DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/096,762 FILING DATE: 22-JUL-1993
                                                                                       APPLICATION NUMBER: FILING DATE: 07-DE
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03-DEC-1993
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                                    10-OCT-1995
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                                                                                                                                                                                                                      US 08/165,699
                                                        US 08/544,404
                                                                                                                                                                US 08/209,741
                                                                                                              US 08/352,322
     US 08/728,463
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: V
FILING DATE: 10-OCT-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 10-OCT-
PRIOR APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1216 AGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCA 1275
                                                                                                                                                                                                                                                1516 GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCCGGCGTCAATACGGGATAATACCGCG 1575
                                                                                                                                                                                                                                                                                                               1456 GTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGA 1515
                                                                                                                                                                                                                                                                                                                                                                                 1396 AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1276 CGCTCGTTTTGGTATGGCTTCATTCAGCTCCGGTTCCCCAACGATCAAGGCGAGTTACA 1335
                                                  1696 TCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAAT 1755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 cgctcgtcgtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttaca 180
                                                                                                                361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                                              301 gtcatgccatccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctga 360
                                                                                                                                                                                                                                                                                                                                                                                                241 agtaagttggccgcagtgttatcactcatggttattggcagcactgcataattctcttact 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Apple, Randolph T. REGISTRATION NUMBER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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601 gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttccttttt 660
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                                                                   tetteageatettttaettteaecagegtttetgggtgageaaaaacaggaaggcaaaat 600
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02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: WO PCT/US96/16433
10-OCT-1996
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US-08-758-417A-217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1876 ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1756 GCCGCAAAAAAGGGGAATAAGGGGCGACACGGAAATGTTGAATACTCATACTCTTTCCTTTTT 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lonberg, Nils
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                   APPLICATION NUMBER: US 08/053,131 FILING DATE: 26-APR-1993
                                                  APPLICATION NUMBER: US 08/096,762 FILING DATE: 22-JUL-1993
                                                                                        APPLICATION NUMBER: US 08/155,301 FILING DATE: 18-NOV-1993
                                                                                                                               APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec_1996
                                                                                                                                                                                                     APPLICATION NUMBER: US 08/209,741 FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/728,463 FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
     APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Crew LLP
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 NUMBER: US
                                                                                                                             03-DEC-1993
07/990,860
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; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: DNA ; SEQUENCE DESCRIPTION: SEQ ID NO: 217: US-08-758-417A-217
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                 721 atttagaaaataaacaaataggggttccgcgcacatttccccgaaaagtgccacctgac 780
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                                                                                                                                                                                                gccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactctttccttttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcg 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACATAGCAGAACTTTAAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTC
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LENGTH: 3881 base pairs
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TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER: 014643-009030US
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                                                           Query Match
Best Local
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Patent No. 6225042
                                                   Matches
                                                                                                                                                                                   TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS: LENGTH: 3883 base pairs
                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OLSON, AIRE M.
REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSKI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM; PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
     2499
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 16-MAR-19:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Brunmark, Anders
APPLICANT: Jackson, Michael
APPLICANT: Peterson, Per A
TITLE OF INVENTION: ANTIGEN PRESENTING
NUMBER OF SEQUENCES: 59
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                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cai, Zeling APPLICANT: Sprent, Jonathan
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STREET: 20 No. 6
CITY: Chicago
STATE: Illinois
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                                                         Local
                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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                                                           Similarity
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Application US/09039982A
225042
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E: Olson & Hierl; Ltd.
20 No. 6225042th.Wacker Drive,
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                                             Score 1001; DB 4; I
Pred. No. 2.4e-301;
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                                                                     Length 3883;
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Sequence 30, Application US/09039641
Patent No. 6551627
GENERAL INFORMATION:
APPLICANT: Cal, Zeling
APPLICANT: Sprent, Jonathan
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; ANTI-SENSE: US-09-039-641-30
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REGISTRATION NUMBER: 30,203
REFERENCE/DOCKET NUMBER: TSRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 580-1180
TELEFAX: (312) 580-1189
INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jackson,
APPLICANT: Peterson,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                               2499
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
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LENGTH: 3883 base pairs .
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NAME: Olson, Arne M.
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 2139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 20 NO.
CITY: Chicago
STATE: Illinoi.
COUNTRY: USA
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                 361 gaatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacgggataataccgcg
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/
FILING DATE: 8-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                              CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 2440
GAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCG
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20 No. 6251627th Wacker Drive,
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Jackson, Michael
Peterson, Per A
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SUMMARIES

BASE COUNT ORIGIN

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Couto, L.B., Colosi, P.C. and Qian, X.
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Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated vectors for expres
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Sequence 13 from patent
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                                                                                            Patent: US 6221349-A 13 24-APR-2001;
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                                                         Sequence 1 from patent US 6130203.
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Hybrid proteins with modified activity
Patent: US 6130203-A 1 10-0CT-2000;
Patent: Location/Qualifiers
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Complete cDNA encoding human factor VIII.
E00527
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8831) Danieru, J.K., Richiyaado, M.R., Goodon, A.B. and Uiriamu, A.U. MANUFACTURE OF FUNCTIONAL VIII FACTOR
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Homo sapiens
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JP 1985243023-A/2.
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GENEMTECH INC
OS Homo Sapiens
PN JP 1985243023-A/2
PD 03-DEC-1985
PF 19-APR-1984 US 84
PI DANIERU JIEFURII KEIPON
AREN BIHHAA,
PI UIRIAMU AAUIN UTSUDO
PC A61K37/04,A61K35/12,A61
PC C12N15/00//C12P21/00.(C
CC Strandedness: Single;
PC topology: Linear;
PC typothetical: NO;
PC anti-sense: NO;
PC anti-sense: No;
PC *Source: Cell_line=CH-2
PC *Source: Chromosome/see
PH Key Incatic
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PT Sig_Peptide 110. 7
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19-APR-1985 JP 1985085295
20-APR-1984 US 84 6023
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Location/Qualifiers
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110. .7265
/product='factor VIII'
7266. .<8967
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Methods of reducing factor viii clearance and compositions therefor Patent: WO 0071714-A 1 30-NOV-2000,
The American National Red Cross (US)
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1 (bases 1 to 8967)
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Sequence 1 from
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KWNEANRPGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTA
FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQRE
                                                                               KEKGAITQSPLSDCLTRSHSIPQANRSPLPIAKVSSFPSIRPIYLTRVLFQDNSSHLP
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TTRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
                                                                                                                  SQQNFVTQRSKRALKQFRLPLEETELEKRIIVDDTSTQWSKNMKHLTPSTLTQIDYNE
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VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY
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KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
AVFDEKSWISETKNSLMQDKDAASARAWPKMITVNGYVNRSLPGLIGCHRKSVYWHV
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/db_xref="GI:12226921"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSH
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APTKDEFDCKAMAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
IFDETKSWYFTENMERNCRAPCNIQMEDPTFKENYRFHAINGYLMDTLDGLVMAQDQR
IRWYLLSMGSNENIHSIHFSGHVFTVRKKEFXKMALYNLYPGVFETVEMLPESKAGIWR
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                             DSFTPVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY" 167. .7162
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                                                                                                                                                             AAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAAGAAGAAGATGATA
                                                                                                                                                                                            CACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTTGGTGTATCCTACTGGA
                                                                                                                              AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA
                                                                                               TGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAAG
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SOURCE

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GI:3007544

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Sequence 1 from patent US 171409

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Retroviral delivery of full length factor VIII
Patent: US 5681746-A 1 28-OCT-1997;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 8967) Wood, W.I., Capon, D.J., Simonsen, C.C., Eaton, D.L., Gitschier, J.,
                                                     Homo sapiens
                                                                                        X01179.1 GI:31498
                                                                                                               Human mRNA for
                                                                           factor VIII; signal peptide
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TITLE
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COMMENT
BASE COUNT
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SYEDISAYLLSKNINA IEBRSESONSRHSSTROKOFNATTI PERDIEKTDPWFAHRTPM
PKIQNYSSOLLMLLRQSPTPHGLSLLSDLQEAKYETFSDPSPGAIDSNINLTST 19ESDNISASCOKNYGDYYED
PKIQNYSSSDLLMLLRQSPTPHGLSLSDLQEAKYETFSDPSPGAIDSNINLTST 19ESDNIA
AGTDNITSSLGPSMPHYDSOLDTILFGKKSSPLTESGGPLSLSEENNDSKLLESGLM
NSQESSWGKNYSSTESGRLFKGKRAHGFALLTKNALFKYSISLLKTINLTST 19ESDNLA
AGTDNITSSLGPSMPHYDSOLDTILFGKKSSPLTESGGPLSLKTINLTST 19ESDNLA
NSQESSWGKNYSSTESGRLFKGKRAHGFALLTKNALFKYSISLLKTINLTSNUSATIR
KTHIDGPSLLIENSPSYWONILESDTEFFKYPPLIHDBHLMDKNATALRCHNHSNKTT
SSKNMEMVQQKKEGPIPPDAQNPDMSFFKNIFLPESARWIQRTHGKNSLNSGQGPSPK
QLVSLGPEKSVEGQRELSEKNKYVVGKGFFKNPKNLFLLSTRONUSGSYDGA
YAPVLQDFRSLLIENSFSYWONILESDTEFKKYPPLHDBHLMDKNATALRCHNHSNKTT
SSKNMEMVQQKKEGPIPPDAQNPDMSFFKNDFLEBGLGNOTKQIVEKYACTTRISPNT
SQNIFYTQRSKALKQFRLPLEFELEKRIITODDKSKNMKHLFPSTLTOIDYNP
KEKGATTQSPLSDCLTRRHSIPPLAKFSKFSPSIRPIYLTRVLFQDNSSHLP
ANSYRKKDSGVQESSHFLQGAKKNNLSLAILTLEMGDQREVGSLGSGESDLOGSTRAK
EKKGATTQSPLSDCLTRRHSIPPLAKFSFPSIRPIYLTRVLFQDNSSHLP
ANSYRKKDSGVQESSHFLQGAKKNNLSLAILTLEMGNDHYGTQIPKEEWKSQEKSPEKTA
FKKDTILSLNACESNIAIAALNEGQNKPEIEVTWAKGGRTEELCSQNEPVLKRHQRE
ITRTTLQSDLODETISVEMKKEDEDIYDEDENGSFRSQKKTRHYFIAAVERLH
DYGMSSSPHVLRNAQSGSVPQFKKVVEQETFDGSFTQPLYRGELLGRYIRA
EVEDNIAWTFRNQASRFYSFYSSLISYEEDQRGAEFRKNEFVKPHERGLCTGCALFYIRA
EVEDNIAWTFRNQASRFYSFYSSLISYEEDQRGAEFRKNEFVKPHERGROVTVQEFALFFT
IFDETKSWTFTENMERRCRAPCNIQMEDFTFKNYTRTHAHGRIAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTHMALAGTH
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                                                                                                          /note="polyadenylation signal"
8967
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VECLIGEHLHAGMSTLFLVYSNKCQTPLGMASGHIRDFQITASGQYGQWAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKFSSLYISQFIIWYSLDGKKWQ
                                                                                                                                                                                                                                                 /note="3
                                                                                                                                                                                                                                                                                                                                                                                                                                 DSFTBVVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEW
LQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {	t TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL}
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RLPKGVKHLKOFPILFGEIFKYKWTVTVEDGFTKSDFRCIFRYSGTVNNERDLASGL
IGPLLICYKBSVDQRGNOIMSDKRNYLLFSVFDENRSWYLTENIQRFLPUPBAVOLED
DEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDFLSVFFSGYTFKHKMV
                                                                     /notex"polyA site"
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/db_xref="taxon:9606"
<1...109
                                                                                                                                                                                                                                                                                                                                              /product="mature factor VIII (aa 1-2332)"
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VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY
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VDARFPPRVPKSFPFNTSVVYKKTLFVEFTDHLFNIAKPRPPMMGLLGPTIQAEVYDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGMGTTPETHSIFLEGHTFLVRNHRQASLEISPITFLTAQTLLMDLGQFLLFCHISSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aagtetteeetggtggaageeataeatatgtetggeaggteetgaaagagaatggteeaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgttatcctactgga
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                                                                                       Truett, M.A., Blacher, R.W., Burke, R.L., Caput, D., Chu, C., Dina, D., Hartog, K., Kuo, C.H., Masiarz, F.R., Merryweather, J.P., Najarian, R., Pachl, C., Potter, S.J., Puma, J., Quiroga, M., Rall, L.B., Randolph, A., Urdea, M.S., Valenzuela, P., Dahl, H.-H.M., Favalaro, J., Hansen, J., Nordfang, O. and Ezban, M.
                                                        Characterization of the polypeptide composition of human factor {\tt VIII:C} and the nucleotide sequence and expression of the human
                           DNA 4 (5), 333-349 (1985)
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 9029)
                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                            Human kidney, cDNA to mRNA, clones pF8[100,102]; and cell line GM1416 DNA, clone pF8-4.3.
                                                                                                                                                                                                                                                                              coagulation factor VIII:C
                                                                                                                                                                                                                                                                                              M14113
M14113.1 GI:182817
                                                                                                                                                                                                                                                                                                                           Human coagulation factor VIII:C mRNA, complete cds
                                            kidney cDNA
                                                                                                                                                                                                                                                                                                                                                 HUMFVIIIC
(sites)
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                                                                                                                                                                                                                                                                                                                                             mRNA
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Draft entry and clean copy sequence for [1] kindly provided by M.A.Truett 26-FEB-1986.
The mutation at position incomparison in the mutation at position in the mutation in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88197150
[3] site
[2] site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Youssoufian, H., Wong, C., Aronis, S., Platokoukis, H., Kazazian, H.H. Jr. and Antonarakis, S.E. Moderately severe Memophilia A resulting from Glu----Gly substitution in exon 7 of the factor VIII gene Am. J. Hum. Genet. 42 (6), 867-871 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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DeRosa,V. and Marchetti,G.
A HINDIII RFLP and a gene lesion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The mutation at position 1042 results in a change of Glu to and the one at position 1043 in a change from Glu to Gly. T mutation at position 1042 produces a premature stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (sites)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDETFKTREAIOHESGILGPLLYGEVGDTLLIIFKNQÄSRPVNIYPHGITDVRPLYSR
RLÞKGVKHLKDPPILRGEIFKYKWTVTEOHDFRKTSRYLSSFVNMERDLASGL
IGPLLICYKESVDQRGNÓIMSDKRNVLIFSVEDENRSNYLTENIGRFLANGOLED
PEFQASNIMHSINGYVFDSLQLSVCLHEVAYWYILSIGAQTDPLSVFFSGYTFKHKMV
YEDTLTILFPFSGETVFMSMENPGLWILGCHNSDFRNRGMTALLKVSSCDKNTGDYYED
SYEDLSAYLLSKNNA LEFRSFSONSKHPSTROKOFNATTI PENDIEKTDWFAHATPM
PKIQNVSSSDLLMLLRQSFTPHGLSLSDLQEAKYETFSDDPSPGAIDSNNSLSEMTHF
RQQLHHSGDMVTTPESGIQLRLMEKLGTAATELKKLDFKVSSTSNNLISTIPSDNLA
AGTDNTSSLGEPSMPWYDSOLDTILFGKKSSPLTESGGPLSLSEENNDSKLLESGLN
NSQESSWGKNVSSTESGRLFKGKRAHGPALLTKDNALFKVSISLLKTNKTSNNSATNR
                                                                                                                                                                                                                                                                                                                                                                                 KTHIDGPSILIENSPSVWQNILESDTEFKKVTPLIHDRMLMDKNATALRINHMSNKTT SSKNMEMVQQKKEGP IPDDAQNEDMSFFKMLFLPESARRIQRTHGKNSLNSGQDSPK OLVSLAPEKSVEGQNELESKINKVVCKKCEFTKDVGLKEMVFPSSRNLFITULDUNLEN NTHNQEKKIQEEEKKKLTLIQENVLLPOIHTVTGTKNFMKNLFLLSTRQNVEGSYDGA YAPVLQDFSCMSTRHFKKHTAHFSKGEEBMLEGLGWQTKQLVEKYACTTRISPNT SQONWTYGRSKRALKOFELPLEETELEKRIIVDDTSTQMSKNMKHLTFSTLTQLDVMSK SGEKGAITQSPLSDCLTRSHSIPQANRSPLPIAKVSSFPSIRPIYLTRVLFQDNSSHLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVFDEGKSMISETKNSLMODADAASARAWPKHITVNGYVNRSLPGLIGCHRKSYVWHV
IGMGTTPEVHSIFLEGHTFLVRNHRQASLEISPITFLTAGYTLLMDLGGFLLFCHISSH
QHDGMEAYVKVDSCPEEPQLHMKNNEEAEDVDDDLTDSEMDVVRFDDDDSPSFTQIRS
VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFMAY
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VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
                                             FKKKDTILSLNACESNHAIAAINEGQNKPEIEVTWAKQGRTERLCSQNPPVLKRHQRE
ITRTTLQSDQEEIDYDDTISVEMKKEDFDIYDEDENQSPRSFQKKTRHYFIAAVERLW
DYGMSSSPHVLRNRAQSGSVPQFKKVVFQEFTDGSFTQPLYRGELNEHJGLLGFYIRA
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/protein_id="AAA52485.1"
/db_xref="GI:182818"
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172. .228'
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/db_xref="taxon:9606"
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EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
                                                                                                                                                                                                                  KWNEANRPGKVPFLRVATESSAKTPSKLLDPLAWDNHYGTQIPKEEWKSQEKSPEKTA
                                                                                                                                                                                                                                                                                 ENTVLPKPDLPKTSGKVELLPKVHIYQKDLFPTETSNGSPGHLDLVEGSLLQGTEGAI
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                                                                                                                                                                                                                                                                                                                              \mathtt{AASYRKKDSGVQESSHFLQGAKKNNLSLAILTLEMTGDQREVGSLGTSATNSVTYKKV}
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Lollar, J.S. and Runge, M.S.
Hybrid human/animal factor VIII
Patent: US 5744446-A 1 28-APR-1998;
Location/Qualifiers
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Modified factor VIII
Patent: US 5859204-A 1 12-JAN-1999;
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Lollar, J.S.
Modified factor VIII
Patent: Us 6180371-A 1 30-JAN-2001;
Location/Qualifiers
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AL598454	в84895	AG009622	7	AV404393	AG007414	AG013813	AG010296	AG004170	AG016243	AG000533	BG923556	AG014348	AV601733	BG923768	AG008943	AG001126	AL044583	в07159	BG838185	AL041936	AV612734	AG002706	AL599532	AZ918759	CNS075W1	AV611386	AL046135	AG010947	AG000534	AL041808	BE569687	BE573230
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ALIGNMENTS

RESULT

FEATURES SOUICE	JOURNAL COMMENT	TITLE	REFERENCE AUTHORS	KEYWORUS SOURCE ORGANISM	z	BG838279/c LOCUS DEFINITION
	Unpublished (2001) Contact: Singh,J.A. Eastern Cereal and Oilseed Research Centre	.N.A. EXPRESSED Sequence Tags from Cold-Stressed Glycine clandestina Seedlings	Glycine. (bases 1 to 935) Singh,J.A., Farah,S., Chapados,J., Couroux,P., De Moors,A., Harris, L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,	EST. Glycine clandestina. Glycine clandestina Glycine clandestina Glycine clandestina Glycine clandestina Embryophyta; Tracheophyta; Embryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;	BG838279 BG838279.1 GI:14204601	BG838279 935 bp mRNA EST 25-MAY-2001 GC01_10e07_R Gc01_AAFC_ECORC_cold_stressed_Glycine_clandestina Glycine_clandestina cDNA clone Gc01_10e07, mRNA sequence.

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                                                               TATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCCGAAAAGTGCCACCTAA
                                                                                                                                     TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG
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                                                                           agtaagttggccgcagtgttatcactcatggttattggcagcactgcataattctcttact
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                                                          AGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACT
                                                                                                                                      TGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGA
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                                                                                                                                                                                                                                                                                                                                                                     CCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGT 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone (DKFZp434E111) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heidelberg/Germany) within the cDNA sequencing German Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: poustka@mpimg-berlin-dahlem.mpg.de
This is the 5' sequence of the clone Insert
Clone from S. Wiemann, Molecular Genome Analysis, German Can-
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +49-30-84131623
Fax: +49-30-84131128
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DKFZp434E111 5', mRNA sequence.
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Innestrasse 73, 14195 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department Lehrach
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST (Poustka, et al.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poustka, A., Klein, M., Mewes, H.W.,
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1 (bases 1 to 841)
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192 c 202 g 221 t
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="DKFZp434E111"
/clone_lib="434 (synonym: htes3)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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BG920379
BG920379.1 GI:14300855
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                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.lln#.gov
                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                               quality sequence start: 15 quality sequence stop: 717.
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator
                                                                  /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="Infiltrating ductal carcinoma"
/dev_stage="5 months"
                                                                                                                                                             /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                  Location/Qualifiers
                                                     /lab_host="DH10B"
                                                                                                                                            /clone="IMAGE:4954975"
                                                                                                                                                                                                 /organism="Mus musculus"
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                                                      AL040542 767 bp mRNA
DKFZp434I1114_r1 434 (synonym: h
DKFZp434I1114 5', mRNA sequence.
AL040542
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Eukaryota; Metazoa;
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                                             AL040542.1 GI:5409490
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96.5%;
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671 gaagcatttatcagggttattgtctcatgagcggatacatatttgaatgtatttagaaaa 730
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                                                                                                                                                                                                                                    GAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCT 406
                                  taccgctgttgagatccagftcgatgtaacccactcgtgcacccaactgatcttcagcat 550
                                                                                                                                                                                                                                                                                                                                                                                        | ccgtaagatgcttttctgtgactggtgagtactcaaccaagtcattctgagaatagtgta 370
                                                                                                                                                                                                                                                       gaactttaaaagtgctcatcattggaaaacgttcttcggggcgaaaactctctaaggatct 490
                                                                                                                                                                                                                                                                                                                                                                     CCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
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This is the 5' sequence of the clone insert
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/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
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602 ccgcaaaaaagggaataagggcgacacggaaatgttgaatactcatactcttcctttttc
                                                        505 CTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATG 446
                                                                                                                                                                                                                                                                                                                   362 aatagtgtatgcggcgaccgagttgctcttgcccggcgtcaatacggggataataccgcgc 421
                                                                               542 cttcagcatcttttactttcaccagcgtttctgggtgagcaaaaacaggaaggcaaaatg
                                                                                                                                      565 CAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGAT 506
                                                                                                                                                          482 caaggatettaeegetgttgagateeagttegatgtaaeeeaactegtgeaeeeaactgat 541
                                                                                                                                                                                                                 625 CACATAGCAGANCTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCT
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                                                                                                                                                                                                                                                                                            685 AATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGNATAATACCGCGC
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s. Wiemann@dkfz- heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No s1 sequence available. This clone (DKFZp31301920) is available at the RZPD in Berlin
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Contact: Duesterhoeft A
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/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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/db_xref="taxon:9606"
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99.7%;
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Pred. No. 1.9e-172;
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Matches 639;
                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Am Klopferspitz 18a D-82152 Martinsried, Germany
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s. Wiemann@dkfz heidelberg.de;
Research Center (DKF2); Email s. Wiemann@dkfz heidelberg.de;
sequenced by LMU (Ludwig Maximilians University,
sequenced by LMU (Ludwig Maximilians University)
                                                                                                                                                                                                                                                                                                                                                                         No s1 sequence available.
This clone (DKFZp434M0421) is available at the RZPD in Berlin please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Munich/Germany) within the cDNA sequencing consortium of the German
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                               Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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    Conservative
                                                                                                                                                                                   /clone="DKFZD434M0421"
/clone_lib="434 (synonym:
/tissue_type="testis"
/dev_stage="adult"
                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                    /lab_host="DH10B"
                          63.6%;
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                          Score 636.6; DB 10 Pred. No. 4.7e-172;
          Mismatches
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                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                        TITLE
                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 TGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAAGTG
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1. (bases 1 to 914)
                                                                                                                                                                                                                                                                                                                                                               BE569261 914 bp IIRNA
601331179F1 NCI_CGAP_Mam6 Mus
                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
             found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM8928 row: m column: 20
                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                 BE569261.1 GI:9812981
                                                                                                                                                                                                                                                                                    house mouse
                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can
quality sequence stop: 685
                                                                                                                                                                                                                                                                                                                                                                                  914 bp
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                                                                                                                                                                                                               ATGAGCGGATACATATTTGAATGTATTAAGAAAATAAACAAATAGGGGTTCCGCGCACA
                                                                                                                                                                                                                                       atgagcggatacatatttgaatgtatttagaaaaataaaacaaataggggttccgcgcaca 756
                                                                                                                                                                                                                                                                                          TGAATACTCATACTCTTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTC
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AL042540 702 bp mRNA EST 29-FEB-2000 DKFZP434I1621_r1 434 (Synonym: htes3) Homo sapiens cDNA clone DKFZP434I1621 5', mRNA sequence.
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a 207 c 199 g 233 t
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/clone_lib="NCT_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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281 AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGC
                      546 agcatcttttactttcaccagcgtttctgggtgagcaaaaacagggaaggcaaaatgccgc 605
                                                                                    341 GATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
                                                                                                                                                                      401 TAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGGCGAAAACTCTCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         641 CCATGTTGTGCAAAAAAGCGGTTAGCTCNTTCGGTCCTCCGATCGGTTGTCAGAAGTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 ccatgttgtgcaaaaaagcggttagctccttcggtcctccgatc-gttgtcagaagtaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             701 GTATGGGCTTCCATTCAAGCTCCCGGTTCCCCAACGATCAAGGCGAAGTTACATGATCCC 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 gtttggtatggcttcattcagctccggttcccgacgatcaaggcg-agttacatgatccc 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity es 637; Conserv
                                                                                                                                                                                                                                                           GTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACA
                                                                                                                                                                                                                                                                                    9t9tat9c9gcgaccgagttgctcttgcccggcgtcaatacggggataataccgcgccaca 425
                                                                                                                9atcttaccgctgttgagatccagttcgatgtaacccactcgtgcacccaactgatcttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCAATAATTCTCTTACTGTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No s1 sequence available.
This clone (DRFZp434I1621) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Am Klopferspitz 18a D-82152 Martinsried, Gormany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berlin-Charlottenburg, GERMAN Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 702)
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/lab_host="0H10B"
/note="Vector: pSport1;
/note="Vector: pSport1;
159 c 164 g 1;
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/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
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96.2%;
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Pred. No. 4.7e-159;
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192 t 2 others
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515 CCATGTTGTGCAAAAAGCGGTTAGCCTCTTCGGTCCTCCGATCGTTGTCAG-AGTAAGTT 457
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                                                                             gtttggtatggcttcattcagctccggttcccaacgatcaaggcgagttacatgatcccc 188
                                                                                                           AGTTAATAGTTTGCCCAACGTTGTTGCCAATGCTACAGGCATCGTGGTGTCACGCTCGTC 576
                                                                                                                        agttaatagtttgcg@aacgttgttgccattgctacaggcatcgtggtgtcacgctcgtc 128
                                                       Homo sapiens genomic DNA, 21q region, clone: PQ624A20, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Hattori,M., Ishii,K., Shiba,T. and Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (10-NOV-1997) to the DDBJ/EMBL/GenBank databases
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/db_xref="taxon:9606"
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95.1%;
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Pred. No. 3.9e-158;
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GSS.
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                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-SEP-1998) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, Kitasato University, Department of Science,
Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens DNA, clone:B335C24BB28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 658)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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96.5%;
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                                                                                        Score 576.8; DB 13; Pred. No. 7.3e-155;
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Submitted (31-OCT-1997) to the DDBJ/EMBL/GenBank databases
Masahira Hattori, Kitasato University, Department of Science, JST
Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan
(E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732,
                                                                                                                    2 (bases 1 to 793)
Hattori,M., Ishii,K., Shiba,T. and Sakaki,
Homo sapiens ganomic DNA, chromosome 21q
Published Only in DataBase (1997) In press
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1 (bases 1 to 793)
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/chromosome="21"
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Submitted (06-JUL-1998) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, Kitasato University, Department of Scienc Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Jap
                                                        Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y. Direct Submission
                                                                             Published Only in DataBase (1998) In press 2 (bases 1 to 696)
                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 696)
                                                                                                                                                                                                                                              survey sequence.
AG009765 AG00357
AG009765.1 GI:3
                                                                                                                 Hattori, M., Ishii, K., Toyoda, A., Shiba, T. and Sakaki, Y. Homo sapiens genomic DNA, chromosome 21g
                                                                                                                                                                                Eukaryota;
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                                                                                                                                                                                TGATCTTCAGCATCTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAAC
                                                                                                                                                                                                                             CTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAC
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Eukaryota; Metazoa;
Mammalia; Eutheria;
l (bases 1 to 696)
                                                                                                       BE573230 696 bp mRNA
601333125F2 NCI_CGAP_Mam6 Mu:
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On Feb 5. 1999 this sequence version replaced AG003576: Submitted (19-Dec-1997)
                                                            EST
                                                                                 mRNA sequence.
BE573230
                                   Mus musculus
                                                                       BE573230.1 GI:9816950
                                                nouse mouse.
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165 c
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/db_xref="taxon:9606"
/chromosome="21"
/clone="P8G4SpN15"
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99.5%;
           Chordata;
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Pred. No. 2.6e-148;
0; Mismatches 0;
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          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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les 615; Conservative
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AAATGTTGAATACTCATACTCTTTCCTTTTTCAATATTA-TGAAGCATTTATCAGGGTTA-
                      TGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAAGTGCTCATC
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Tissue Procurement: Jeffrey_Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg,
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: NotI; Cloned unidirectionally. Primer: Olig
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/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
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/db_xref="taxon:10090"
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               ccgatcgttgtcagaagtaagttggccgcagtgttatcactcatggttatggcagcactg
                                            TCAAGGCGAGTTACATGATCCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCT
698;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
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Contact: Robert St
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 801)
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Location/Qualifiers
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National Institutes of Health, Mammalian Gene Collection (MGC)
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nilarity 94.3%;
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Site_2: NotI; Cloned unidirectionally. Prim
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/sex="female, virgin"
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/dev_stage="5 months"
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/clone="IMAGE:3709789"
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                                                                                        Please contact the RZPD:
                                                                                                                                                                                                                                                                                                                                                       human
    /db_xref="taxon:9606"
/clone="DKFZp434B0518"
                               /organism="Homo sapiens"
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598 TACTCCATACTCTTTTTCAAGTATTTATCGAAGCATTTCATCATGGCCTC
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                                                                                                                            This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz- heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No sl sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL041808 554 bp mRNA EST 29-FEB-2000 DKFZP434B0518_rl 434 (synonym: htes3) Homo sapiens cDNA clone DKFZP434B0518 5', mRNA sequence.
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Berlin- Charlottenburg, GERMANY; Email:
    Location/Qualifiers
                                                                              This clone (DKFZp434B0518) is available at the RZPD in Berlin
                                                      Ressourcenzentrum, Heubnerweg
                             clone@rzpd.de
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Best Local Similarity 99.3%;
Matches 548; Conservative
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       aaagtgccacct 777
                                                                        TACATATTTGAATGTATTTAGAAAAATAACCAAATAGGGGTTCCGCGCACATTTCGCCGA
                                              tacatatttgaatgtatttagaaaaataaacaaataggggttccgcgcgcacatttccccga
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="9H10B"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
a 123 c 124 g 155 t
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Search completed: January Job time: 4792 sec

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1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT:*

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Listing first 45 summaries
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(without alignments)
1999.219 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AAF84648	AAV12112	AAV23339	AAN80444	AAN90654	AAN80446	AAN80447	AAX82258	AAN50375	AAT73164	AAQ76016	AAX88293	AAQ66615	AAA49231	AAN81544	AAN60689	AAT51357	AAV18884	AAN81096	AAN81439	AAT03571	AAX82260	AAX82261	AAX82259	AAC90508	AAX91162	AAV25810	AAT61548	AAQ50185	AAV19580	AAV15359	AAF60309	AAZ38604	AAN50054
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ALIGNMENTS

RESULT AAD00122

ببز

AAD00122 standard; DNA; 4999 BP

AAD00122;

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20-OCT-1998;
24-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                       Recombinant Adeno Associated Vector; rAAV; pVm4.1cF8deltaB; promoter; human Factor VIII; hFVIII; EF1alpha; human elongation factor-lalpha; human growth hormone; hGH; ITR; inverted terminal repeat; haemophilia;
                                                                                                                                                                                                                                                                                     Recombinant adeno associated vector construct, pVm4.1cF8deltaB.
                                                                                                                                                                                                                                                                                                            31-JUL-2000 (first entry)
New recombinant adenovirus-associated vector, useful for gene therapy
                                                                                                                                                            27-APR-2000.
                                                                                                                                                                                                         Adeno associated virus.
                                                                                                                                                                                                                              gene therapy; ds.
                                              Couto LB,
                                                                                                                                     19-OCT-1999;
                                                                                                                                                                                   WO200023116-A1
                       WPI; 2000-339536/29.
                                                                    (AVIG-) AVIGEN INC.
                                              Colosi PC;
                                                                                          98US-0104994.
99US-0125974.
99US-0364862.
                                                                                                                                        99WO-US24495
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to treat hemophilia, comprises at least a operably linked to control sequence -
                               portion of Factor VIII
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9; Fig 6; 92pp; English.

The present DNA sequence is a recombinant adenovirus-associated vector, CC (rAAV) construct pVm4.1cP8deltaB. This expression vector comprises the CC promoter, first intron (-573 to +985) of human elongation factor-lalpha CC (EFlalpha) gene, human Factor VIII coding sequence (hGWIII) and a CC polyadenylation signal from human growth hormone (hGH). This sequence is CC inserted between the AAV inverted terminal repeat (ITR) regions. The CC inserted between the AAV inverted terminal repeat (ITR) regions. The CC inserted between the AAV inverted terminal repeat (ITR) regions. The CC inserted between the AAV inverted terminal peptide, Al and A2 domains CC and 5 maino acids from the N-terminus of the B domain. The light chain CC segment comprises the C-terminal 85 amino acids of B domain and the A3, CC and C2 domains. Both the heavy and light chain segments are cloned CC into the same plasmid seperated by 42 nucleotides coding for 14 residues CC of the B domain, that is deleted. This plasmid is operably linked to CC control sequences, that directs the transcription and translation of the CF factor VIII gene. The adeno-associated viral vectors are used for gene CC therapy, because of factor VIII in vivo. The rAAV are used for gene CC therapy, because of their broad host range, safety profile and duration expression in the infected hosts.

Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other;

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agtcgtgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaa
                                                   gctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttcccattcaacacctc
                                                                                                   aagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtga
                                                                                                                       aagatactacctgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtga
                                                                                                                                                                       aatagagctctccacctgcttctttctgtgcctttttgcgattctgctttagtgccaccag
                                                                                                                                                                                        aatagageteteeacetgettetttetgtgeettttgegattetgetttagtgeeaceag
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                                   gctgcctgtggacgcaagatttcctcctagagtgccaaaatcttttccattcaacacctc
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04-SEP-2001 (first entry)
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                                                                                                                                     cctggtaaaagacttgaattcaggcctcattggagcccta
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Chimeric - Adeno associated Chimeric - Homo sapiens. Chimeric - Unidentified.
                                                                                                                                                                                                                                                           Human factor VIII expressing rAAV vector pVm4.1cF8-B partial sequence
28-JUN-2001
                                            WO200145510-A1.
                                                                                                                                                                             PVm4.1cF8-B;
                                                                                                                                                                                                  blood clotting
                                                                                                                                                                                                                     Recombinant adeno-associated viral vector; rAAV;
                                                                                                                                                                             ds
                                                                                                                                                                                                disorder;
                                                                                                                                                                                              gene therapy; haemophilia
                                                                                                                                                                                                                factor VIII;
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21-DEC-2000; 2000WO-US34925

(AVIG-) AVIGEN INC

22-DEC-1999;

99US-0470618

Couto LB, Colosi PC,

coagulation Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood factor VIII

Fig 6; 90pp; English

second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector i useful in gene therapy for treating haemophilia A in mammals, in suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a The present invention relates to a method for treating a subject

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Pred. No. 4.6e-280;
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                      The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF-3 CC (arbumin promoter, the first intron (-573 to +985) of human elongation CC factor-lalpha (EFIalpha) gene, human Factor VIII coding sequence (hFVIII) CC and polyadenylation signal from human growth hormone (hGH). This sequence is inserted between the AAV inverted terminal repeat (ITR) regions. The CC first 57 bp encoding the 19 amino acid signal peptide, A1 and A2 domains CC and 5 amino acids from the N-terminals of the B domain. The light chain segment comprises the C-terminal 85 amino acids of B domain and the A3. CC control sequences, that directs the transcription and translation of the B domain, that is deleted. This plasmid is operably linked to CC control sequences, that directs the transcription and translation of the Factor VIII gene. The adeno-associated viral vectors are used for gene therapy, because of their broad host range, safety profile and duration of conference of their broad hosts.
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24-MAR-1999;
30-JUL-1999;
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133 actaggggttcctgcggccgcacgcgtggtggcgcggggtaaa-----ctgggaaagt

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ID AAD0
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                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                 Matches 870;
                                                                                                                                                                                                                                                                  second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is useful in gene therapy for treating haemophilia A in mammals, in particular humans. The rAAV vector provides high level and long term expression of biologically active clotting factor VIII in vivo. The present sequence is pAAV-F8-1 vector without the plasmid backbone. It comprises HHF-3 mouse albumin promoter, a synthetic intron based on human elongation factor lalpha (EFIalpha) and immunoglobulin G (19G) intron sequences, B-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both the light and heavy chains of human factor VIII.
                                                                                                                                                                                                                                 Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating blood clotting disorder, especially hemophilia in mammals, administering recombinant adeno-associated vectors which express bloosgulation factor {\tt VIII}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Fig 5; 90pp; English.
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Chimeric - Oryctolagus cuniculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pAAV-F8-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII; blood clotting disorder; gene therapy; haemophilia A; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2001 (first entry)
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                                                                                        13 cagctgcgcgctcgctcgctcactgaggccgcccgggcaaagcccggggcgtcgggcgacc 72
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                  tttggtcgcccggcctcagtgagcgagcgcgcgcgcagagagggagtggccaactccatc 132
                                                                      cagctgcgcgctcgctcactgaggccgccgggcaaagcccgggcgtcgggcgacc 60
tttggtcgcccggcctcagtgagcgagcgagcgcgcagagggagtggccaactccatc 120
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                                                                                                                                                 Conservative
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                                                                                                                                                                73.6%;
86.1%;
                                                                                                                                                0;
                                                                                                                                                           Score 736.2; DB 22
Pred. No. 2.6e-203;
                                                                                                                                              Mismatches 118;
                                                                                                                                                                               DB 22;
                                                                                                                                            Indels 23;
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Adeno-association disorder; ss.
                                                                                                                                     AAF84647 standard; DNA; 7944 BP.
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                               Adeno-associated virus vector; B-domain;
                                                         Plasmid DLZ6 encoding Muman B-domain deleted factor VIII.
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                                                                                                                                                                                                                                                                     gtcctgaaagagaatggtccaatggcctctgacccactgtgccttacctactcatatctt
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                                                                                                                                                                                                             tctcatgtggacctggtaaaagacttgaattcaggcctcattggagcccta 1011
                                                                                     (first entry)
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                                    factor VIII; haemophilia
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                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                    vector. The vector comprises a heterologous nucleotide sequence encoding B-domain deleted factor VIII operably linked with at least one enhancer and at least one promoter. The method results in the production of high titer rAAV vector stocks carrying the B-domain deleted factor VIII transgenes and expression cassettes, which generate adequate titers of virus for in vivo administration. The recombinant vectors are useful for treating haemophilia A, where the liver expresses the encoded B-domain deleted factor VIII, which is secreted into the blood. They are also useful for the treatment of other coagulation disorders. The present sequence encodes a B-domain deleted factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enhancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New recombinant adeno-associated virus vector, useful for treating haemophilia A, comprises heterologous nucleotide sequence encoding B-domain deleted human factor VIII operably linked with liver-preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes a recombinant adeno-associated virus (rAAV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression control element -
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P-PSDB; AAB67959.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 64; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYNC-) UNIV NORTH CAROLINA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2000; 2000WO-US28221
                                                                                                                                                                                                                             Sequence 7944 BP; 2142 A; 1902 C; 1909 G; 1991 T; 0 other;
136 aggggttcctgcgccgcacgcgtggt-ggcgcggggtaaactgggaaagtgatgtcgtg
                                                                                                                                                       Local Similarity nes 785; Conserv
                                                                                              15 ctgcgcgctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccgggcttt 74
                                                                                                              16 ctgcgcgctcgctcgctcactgaggccgcccgggcaaagcccggggcgtcggggcgaccttt 75
                                          75
                                                                      76
                                       gcccgggcgcctcagtgagcgagcgagcgcgcagagagggagtggccaactccatcact
                                                  Conservative
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/note= "TK polyA sequence"
4916..5084
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/note= "human B-domain deleted factor VIII"
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/note= "hepatitis B virus EnhI enhancer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burstein H,
                                                                                                                                                                         64.0%;
79.3%;
                                                                                                                                                            0;
                                                                                                                                                                         Score 640; DB 22;
Pred. No. 1.8e-175;
                                                                                                                                                               Mismatches
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                                                                                                                                                               200;
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Hemostatic; antianemic; antidiabetic; nootropic; neuroprotective; vector; osteopathic; antisickling; immunostimulant; gene therapy; collage; endothelial cell; peripheral blood; buffy coat cell; VEGF; PCR primer; vascular endothelial growth factor; bovine brain extract; haemophilia; Factor VIII; human; transgene; adenosine deaminase deficiency; ss;
                                                                                                                                                                                                                                                                    AAA49232 standard; DNA; 12445
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                                                                                                                                     for transforming endothelial cells.
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The invention relates to a method for expanding the population of CC endothelial cells (EC) obtained from peripheral blood, by culturing, CC in contact with a collagen I coated surface, buffy coat cells obtained CC from peripheral mammalian blood in the presence of a culture medium CC containing vascular endothelial growth factor (VEGF) and free of bovine brain extract. EC are useful for treating hemophilia by introducing it CC into the blood stream of a mammal, so that an effective amount of CC fractor VIII protein is secreted in the blood stream of the mammal. CC This sequence represents the vector HSQReNeo where the human factor CC VIII gene into which an enhanced green fluorescent protein coding CC sequence (HSQ) has been inserted, is subcloned. Transgenic EC transduced in vitro are useful for improving prosthetic implants. EC is also useful for diagnosing clotting disorders where indication or disease is CC associated with a reduction in the activity of an enzyme. EC is also useful in gene therapy for treating the variety of diseases including adenosine deaminase deficiency, stokle cell anemia, thalassemia, hemophilia, diabetes, alpha-antitrypsin deficiency, brain disorders such as alzheimer's disease, heart diseases, defects in immune system, for remaining home fractivities and to treat or remaining the content of the cell and the immune system, for remaining home fractivities and to treat or remaining the content of the content of
Sequence 12445 BP; 3255 A; 2989 C; 2951 G; 3250 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expanding population of endothelial cells useful to biocompatibilize implantable medical devices comprises contacting buffy coat cells with collagen I coated surface in culture medium comprising vascular endothelial growth factor -
                                                  for repairing bone fractures and to treat or prevent osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fracture; osteoporosis.
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blood clotting; procoagulant; anticoagulant; antithrombotic;
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donor anticoagulant \Phi_{\mathbf{P}} antithrombotic protein of coagulation disorders
                    Hybrid Factor VIII with modified activity, comprises region from donor anticoagulanton antithrombotic protein - useful for treats
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2225..2314
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AAV19581 standard; cDNA; 4832

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                                                                                 606
                                                                                                                                                      546
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0;

Human factor VIII beta-domain deleted SQN deletion cDNA sequence

06-AUG-1998

(first entry)

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CC intravenously to a human The long term systemic expression results in a CC measurable level of the therapeutic protein being produced in the blood CC of the human for a period of at least 30 days after the administration of CC the RRV vector preparation. RRV's can be used for in vivo delivery of CC thrombosis, hypercoagulable disorders, liver diseases such as hepatitis, CC disorders such as thalassemia, phenylketonuria, Lesch-Nyhan syndrome, CC exerce combined immunodeficiency (SCID), cystic fibrosis, Duchenne's CC diabetes, hypopituitarism, adenine deamlnase deficiency, Juherited emphysema, familial hypercholesterolemia, CC diabetes, hypopituitarism, adenine deamlnase deficiency, alpha1-CC antitrypsin deficiency, Guacher's syndrome, anaemia, infections such as CC inflammatory disease or graft versus host disease, RRV's are capable of Surviving inactivation in human serum thereby allowing efficient gene CC transfer over prolonged periods of time.
                                                              Matches
                                                                                                                                             Sequence 4832 BP; 1381 A; 1089 C; 1055 G; 1307 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressing a therapeutic protein. The RRV preparation is resistant to degradation by human complement and is capable of inducing long term systemic expression of the therapeutic protein when administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This cDNA encodes the beta-domain deleted SQN deletion protein of human factor VIII. This is used in the construction of recombinant retroviral vectors expressing human factor VIII. The invention provides the preparation of replication defective recombinant retrovirus (RRV)
           372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 28; Pages 210-213; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Replication defective; recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; human; hepatitis; thalassemia; phenylketonurla; Lesch-Nyhan syndrome; diabetes; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; hypopituitarism; adenine deaminase deficiency, HIV infection; anaemia; Guacher's syndrome; high blood pressure; Alzheimer's disease, autoimmune;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New replication defective recombinant retro-viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jolly DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUN-1997;
03-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1997;
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                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease;
                                                            605;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VEGA
                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lee R,
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barber JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0869309.
96US-0645601.
96US-0696381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   per JR, Boder M, Chang SMW, Chor
Depolonj, Greengard J, Hsu DC,
R, Mittelstaedt DM, Prussak CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-US11784.
                                                                            59.1%;
96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tactor VIII; ss.
                                                          0;
                                                                        Score 590.6; DB 19
Pred. No. 3.2e-161;
                                                      Mismatches
                                                                                            DB 19;
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Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ibanez CE;
                                                                                          Length 4832;
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RESULT
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          13-AUG-1996;
                       04-JUN-1997;
03-JUL-1996;
                                                          02-JUL-1997;
                                                                                                                                                CDS
                                                                                   08-JAN-1998
                                                                                                         W09800542-A2
                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                          Factor VIII; blood clotting; haemophilia A; gene therapy;
                                                                                                                                                                                                                     retrovirus; vector;
                                                                                                                                                                                                                                                     Human Factor VIII SQN deletion mutant DNA.
                                                                                                                                                                                                                                                                                  20-JUL-1998
                                                                                                                                                                                                                                                                                                                              AAV15338 standard; DNA; 4832 BP
                                                                                                                                                                                                                                                                                                                                                                                                      972 acttgaattcaggcctcattggagcccta 1000
                                                                                                                                                                                                                                                                                                                                                                                        628 acttgaattcaggcctcattggagcccta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caettaagaaeatggetteecateetgteagtetteatgetgttggtgtateetaetgga
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         96US-0696381
                                97US-0869309
                                                         97WO-US11785
                                                                                                                                             Location/Qualifiers 72..4445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pactor VIII, the SQN deletion does not influence the in vivo pharmacokinetics, but the reduced size of the molecule appears to decrease proteolytic degradation. The invention relates to preparations of replication defective recombinant retrovirus (RV) expressing a B domain-deleted human Factor VIII protein, where the recombinant RV is capable of infecting human cells, is resistant to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administered to a haemoghilia A patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA sequence includes a coding region for the B domain deletion mutant SQN (see AAW44372) of human Factor VIII. The SQN mutant is created by fusing Ser-143 to Gln-1638 of native Factor VIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2 vIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2 and A3 Factor VIII domains. When compared to plasmid-derived and A3 Factor VIII domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 174-175; 236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New replication defective recombinant retroviruses - which express domain-deleted human factor VIII or human factor IX for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4832 BP; 1381 Av 1089 C; 1055 G; 1307 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  372 actgacatccactttttctttttctccaccaggtatcgatccaccatgcaaatagagctct 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     432 ccacctgcttctttctgtgcctttttgcgattctgctttagtgccaccagaagatactacc 491
                                                                                                                                                                                                                                328
                                                                                                                                                                                                                                                                                                                          612 aaaagactctgttttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac 671
   508
                 852 aagtottocotggtggaagccatacatatgtotggcaggtootgaaagagaatggtocaa 911
                                                                                                                                                         388
                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg
                                                                               448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccacctgcttcttctgtgccttttgcgattctgctttagtgccaccagaagatactacc
aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa
                                                                                                                                                                                                                                                  cctggatgggtctgcfaggtcctaccatccaggctgaggtttatgatacagtggtcatta 731
                                                                                                                                                                                                                                                                                                        aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac 327
                                                                                                                                                                                                                                                                                                                                                                                acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca
                                                                                                                                                                                                                                                                                                                                                                                                   acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca
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                                                                                               cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga 447
                                                                                                                                                                       cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga 791
                                                                                                                                                                                                                                cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
                                                                           D, Depolo NJ, G
Mittelstaedt DM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.1%;
96.2%;
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NJ, Greengard J, H
t DM, Prussak CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 590.6; DB 19; Length 4832;
Pred. No. 3.2e-161;
0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M, Chong K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Respess JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                              267
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             567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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밁 Qy

Matches Query Match Best Local

605;

Conservative

Similarity

59.1%; 96.2%;

Pred. Score 590.6; Mismatches No.

4.2e-161; DB 17;

Indels

0; Gaps

0

Length 8967;

372 actgacatccactttttctttttctccaccaggtatcgatccaccatgcaaatagagctct 431

66 attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125

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ARESULT
ADAT31031
ID AAT
XX AAT
XX 19-
XXY Fac
XXY Fac
XXY Fac
XXY Fac
XXY HOM
XXY FAC
XXY HOM
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XXY HOM
XXY AT
XXY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT31031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Factor-VIII full-length cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-1996
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                                                                                                                                                                                                                                       A full-length cDNA clone (AAT31031) codes for human Factor-VIII (AAW00465), a trace plasma glycoprotein which acts as a cofactor in conjunction with Factor-IXa in the activation of Factor-X. Retroviral vectors comprising the full-length cDNA can be efficiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-DEC-1994;
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Sequence
                                                                                                                                                                                                        packaged into infectious retroviral particles. These may be used
                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 58-68; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviral vector directing expression of full length factor VIII used in the gene therapy and treatment of haemophilia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW00465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-334010/33.
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      8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chang S,
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167..7
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                   WPI; 2001-025163/03.
                                          Saenko EL,
                                                                                        24-MAY-1999;
                                                                                                             24-MAY-2000; 2000WO-US14111.
                                                                (AMNA-) AMERICAN NAT RED CROSS
                                                                                                                                                           WO200071714-A2
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                      Factor VIII; human; A2 domain; C2 domain; LRP-mediated plasma clearance;
                                                                                                                                                                                                                                                                           13-MAR-2001
                                                                                                                                                                                                    receptor-dependent clearance; receptor-independent clearance;
haemophilia; half-life; ss.
                                                                                                                                                                                                                                                   Human factor VIII cDNA, SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                       AAC87526 standard; DNA; 8967
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          AAB48843
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PT Factor VIII mutants having increased half-life useful for treating PT hemophilia, comprise one or more amino acid substitutions in the A2 XX Claim 41; Page 86-101; 121pp; English.

CC amino acid substitution at one or more positions in the A2 domain and/or an CC amino acid substitution at one or more positions in the C2 domain.

CC amino acid substitution at one or more positions in the C2 domain.

CC amino acid substitution at one or more positions in the C2 domain.

CC amino acid substitution at one or more positions in the C2 domain.

CC amino acid substitution at one or more positions in the C2 domain.

CC amino acid substitution at one or more positions in the C2 domain mutants which lacks a B domain (AB48842). The factor VIII mutants have an increased half-life CC in the bloodstream. The A2 domain mutants exhibit reduced LRP-dependent (receptor approach of factor VIII, while C2 domain mutants to a method of using RAP (receptor associated protein), a protein mutants have related protein), a protein which in the related ligand internalisation, to increase the half-life of factor VIII. The mutant CC internalisation, to increase the half-life of factor VIII. The mutant for treating haemophilia, RAP, LRP-binding RAP mutants or fragments, and nucleotides encoding them, are useful nucleotides encoding them, are useful the invention. The invention provides means of increasing the half-life of factor VIII protein or DNA of the invention. The invention provides means of increasing the half-life of factor VIII protein or DNA of the invention provides means of increasing the half-life of factor VIII.

Sequence 8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;
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В δÃ В 29 Ъ 204 В δÃ DЪ δÃ В 20 g Ş Ъ 20 д δõ Ъ δÃ Matches Query Match 426 186 246 432 ccacctgcttctttctgtgccttttgcgattctgcttttagtgccaccagaagatactacc 491 372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431 66 Local tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga cacttaagaacatggcttcccatcctgtcagtcttcatgctgtttggtgtatcctactgga cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg ccacctgcttcttctgtgccttttgcgattctgctttagtgccaccagaagatactacc acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125 605; Similarity Conservative 59.1%; 0, Score 590.6; DB 22; Pred. No. 4.2e-161; Mismatches Indels Length 8967; 0, Gaps 665 971 605 671 545 851 485 791 425 185 365 305 0

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666 acttgaattcaggcctcattggagcccta 694

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Best Local Similarity
Matches 605; Conserv
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                                                                                                                                                                                                                                                                     The gene encodes human factor VIII. The factor VII is produced in pure form and in useful amts. using recombinant DNA technology. Factor VIII can be used to correct factor VIII deficient plasma, and activates factor X to Xa in the presence of factor IXa, can and phospholipid. These to activities are inactivated by antibodies specific for factor VIII. The activity of the prod. is bound to an immobilised monoclonal antibody specific for factor VIII. Factor VIII activity is activated by thrombin. The activity is bound to, and can be eluted from, immobilised von Willebrand factor. Dose of factor VIII is 20-40 units/kg over 8 hours i.v. for maintenance therapy for haemophilia, 40 units/kg for preoperative conditions, or 15-20 units/kg for minor haemorrhaging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human factor VIII gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human factor VIII; ss cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant functional human factor VIII or deriv. - useful for treating haemophilia and obtd. as pure prod. by recombinant DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-1984;
                                                                                                                                                                                                                                              sequence 8975 BP; 2849 A; 1898 C; 1833 G; 2395 T; 0 other;
                                                                                                                                 372 actgacatccactttttctttttttctccaccaggtatcgatccaccatgcaaatagagctct 431
 186
                                                                                                             66 attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1985-277976/45.
                                                     tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg 551
tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg
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                                                                                                                                                                                       59.1%;
96.2%;
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                                                                                                                                                                         0 * Mismatches
                                                                                                                                                                                        Score 590.6; DB 6; Length 8975; Pred. No. 4.2e-161;
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                                                                                                                   Factor VIII; haemophilia; proteolysis; heavy chain; light chain; secretion; von Willebrand Factor; vWF; C2 domain; intron 22; inv non-functional; bleeding disorder; coagulation; treatment; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ38604 standard; cDNA; 8975 BP.
                                                                                                                                                                                                                                                                                                                                                                  Human full-length factor VIII cDNA.
                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          852 aagtottocotggtggaagccatacatatgtotggcaggtoctgaaagagaaatggtocaa
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                                                                                                                                                                mat_peptide
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                                                                                              W09959622-Al
                                                                                                                                polyA_signal
(GETH ) GENENTECH INC
                         20-MAY-1998;
                                               17-MAY-1999;
                                                                      25-NOV-1999
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                          98US-0082000.
                                                 99WO-US10872
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167..5233
                                                                                                                                /product= "Human factor VIII light chain" 8948..8953
                                                                                                                                                                /product= "Maximum-length human factor VIII heavy chain" 5234..7162
                                                                                                                                                                                                                             110..166
                                                                                                                                                                                                                                       /product= "Human full-length factor VIII"
                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC Known binding sites at the N-terminus and within the C2 domain.

CC Haemophilia A is frequently caused by an intron 22 inversion in the C2 decoming inverted and localised telomeric to two sections, exons 1.22 becoming inverted and localised telomeric to the original site, while C2 exons 23-26 remain isolated at the original site. Exons 23-26 a portion on functional. The factor VIII gene product of individuals with this C2 mutation thus comprises domains, without which factor VIII is CC mutation thus comprises domains A1-A2-B-A3 plus a fragment of C1, which C3 invention relates to a novel method for for treating haemophilia A in a mammal able to produce the factor VIII heavy chain. The method comprises CC light chain, or a gene encoding it, and may be useful for treating cC light chain, or a gene encoding it, and may be useful for treating CC invertion well-characterised starting materials which therefore CC derived from well-characterised starting materials which therefore creduces the risk of pathogenic infection which was previously a problem CC is also a need of providing factor VIII activity to patients who CC factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents cDNA encoding the full-length human factor VIII. In this form, the protein is 300 kD in size with the domain structure Al-A2-B-A3-C1-C2. However, prior to secretion, this 300 kD protein is proteolysed into a heavy chain (Al-A2-B, with continued proteolysis within the B domain resulting in molecules of varying length) and a light chain (A3-C1-C2) that remains non-covalently attached to the heavy chain. Upon secretion, factor VIII is rapidly cleared from the circulation unless it is bound by the plasma protein von Willebrand Factor (VWF). Factor VIII binds to VWF through the light chain, with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8975
                        672 cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
                                                                                   306 aaaagactctgtttgtagaattcacggatcaccttttcaaccatcgctaagccaaggccac 365
                                                                                                                                                                                     246
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                                                                                                                                                                                                                                                                                                                                                                                                                                             372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New method for treating hemophilia
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P-PSDB; AAY52537.
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cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
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                                                                                                                                                                    acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca
                                                                                                                                                                                          acgcaagatttcctcctagagtģccaaaatcttttccattcaacacctcagtcgtgtaca 611
                                                                                                                                                                                                                                                     tgggtgcagtggaactgt&atgggactatatgcaaagtgatctcggtgagctgcctgtgg
                                                                                                                                                                                                                                                                             t999t9cagt9gaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg 551
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                                                                                                                                                                                                                                                                                                                                                              ccacctgcttctttctgtgccttttgcgattctgcttttagtgccaccagaagatactacc 491
                                                                                                                                                                                                                                                                                                                                                                                                                     attaaccttttgcttctccagttgaacatttgtagcaataagtcatgcaaatagagctct 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.1%;
96.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 4.2e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 8975;
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                                                                                                                                                                                                                                                                                                                                          185
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glycerophosphorylserine,

binding is detected. A potential ligand is selected as a potential drug on the basis of its binding to the ligand binding domain of factor VIII with a similar affinity to a standard ligand, such as preferably in conjunction with computer modelling. The potential ligand is contacted with the ligand binding domain of factor VIII and the

phosphate or sulphate.

The method is useful for

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                                                                                                                                                    The present sequence was used in an example illustrating an invention relating to a crystal of protein-ligand complex, which comprises an N-terminal truncated factor VIII and a ligand. The crystal diffracts X-rays to determine the atomic coordinates of the protein-ligand complex to a resolution of more than 5.0 Angstrom. The N-terminal truncated factor VIII retains the C2 domain of, and lacks at least 2000 amino acids from the flexible N-terminus of, the full-length factor VIII. The crystal is useful in drug screening assays. The method comprises selecting a potential ligand by performing structure-based drug design with a three-dimensional structure determined for the crystal in continuation with a continuation with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crystals of protein-ligand complex useful for developing new therapeutic drug agents, comprises carboxy terminal C2 domain of human blood coagulation factor VIII and a ligand -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example; Page 60-64; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; factor VIII; crystal; protein-ligand complex; C2 domain; drug screening; coagulation inhibitor; haemophilia; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9029 BP; 2860 A; 1910 C; 1848 G; 2411 T; 0 other;
                                                                                                                                         AAV15359 standard; DNA;
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                                        Factor VIII; blood clotting;
                                                              Human Factor VIII DNA.
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                         retrovirus; vector; human;
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Pred. No. 4.2e-161;
                                       haemophilia
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                                        A; gene therapy;
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Best Local Similarity
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03-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells, is resistant to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administered to a haemophilia A patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (see AAW44373). The invention relates to preparations of replication defective recombinant retrovirus (RV) expressing a B domain-deleted human Factor VIII protein, such as the SQN deletion mutant (see AAW44372), where the recombinant RV is capable of infecting human AAW44372).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAW44373
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De La Vega
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D, Depolo NJ, Greengard J, Hsu DC, Ib
Mittelstaedt DM, Prussak CE, Respess JG
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Search completed: January 8, 2002, 17:31:47 Job time: 12887 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: January 8, 2002, 17:21:33; Search time 177.22 Seconds (without alignments) 1277.948 Million cell updates/sec

Title: Perfect score: US-09-740-211-14_COPY_1_1000 1000

1 cgcccctgcaggcagctgcg.....caggcctcattggagcccta 1000

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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FILE REFERENCE: AVIGEN-03743
CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1998-10-20
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6221349
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APPLICANT: CO1051, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
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CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 09/364,862
EARLIER FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1998-10-20
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 15
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Best Local Similarity
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TITLE OF INVENTION: by Target Cells
FILE REFERENCE: Avigen,04082
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Matches
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                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                      Local Similarity
les 870; Conserv
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86.1%;
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CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 13
LENGTH: 11933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence 13, Application US/09364862
Patent No. 6221349
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS FILE REFERENCE: AVIGEN-03743
OTHER INFORMATION: Description of Artificial Sequence:
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                                                                                                               Score 736.2; DB 4;
Pred. No. 4.4e-222;
0; Mismatches 118;
                                                                                                                                                     Length 11933;
                                                                                                                   23; Gaps
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RESULT 5
US-08-882-083-1
                                                                                   Sequence 1, Application US/08882083 Patent No. 5869292
                                                                  GENERAL INFORMATION:
   APPLICANT: VOORBERG, Johannes J.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: .17
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 600; Conserv
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
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STREET: 3000 K St.
CITY: Washington
STATE: D.C.
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Pred. No. 8e-177;
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US-08-558-107-1
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TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,107
FILING DATE: 13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VOORBERG, Johannes J: TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: \ 17 CORRESPONDENCE ADDRESS:
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97.9%;
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                                                                                                                                                                             score 592.2; DB 2;
Pred. No. 8e-177;
0; Mismatches 13;
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Patent No. 6130203
GENERAL INFORMATION:
                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/558,107
FILLING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY NUMBER OF SEQUENCES: 17
        SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
                                                              REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/243,539
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                         TELEFAX: 12.
TELEFAX: 904136
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                              STREET: 3000 K St
CITY: Washington
                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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nucleic acid
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                                                                                                                                                          Sequence 1, Application US/08366851A Patent No. 5681746
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                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bodner
APPLICANT: De Pol
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Best Local :
                                                                                           APPLICANT:
                                          CORRESPONDENCE ADDRESS: ADDRESSEE: Viagene,
                                                                               APPLICANT: Chang, Steven TITLE OF INVENTION: Retro
                                                               TITLE OF INVENTION: Retroviral Delivery of Full Length Factor NUMBER OF SEQUENCES: 3 %
  STREET:
CITY: S
STATE:
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TOPOLOGY: lin
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                 San Diego
California 💌 🐧
                       E: Viagene, Inc∴
11055 Rosër⊋e Street
                                                                                                   Bodner, Mordechai
De Polo, Nicolas J.
Hsu, David Chi-Tang
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97.9%;
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Pred. No. 8e-177;
0; Mismatches 13;
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US-08-366-851A-1
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Best Local Similarity
Matches 605; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                     912
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                                                                                                                                                                                                                                                                                                                                               612
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REFERENCE/DOCKET NUMBER: 930049.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/366,851A
                                                                                                              aagettetgagggagetgaatatgatgatcagaecagteaaagggagaaagaagatgata
                                                                                                                                                                              CACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGA
tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                   aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaaatggtccaa
                                                                                                                                                                                                                                                                                                                              aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac
                                                  AAGTCTTCCCTGGTAGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA
                                                                                                                                                                                                                                              CCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTA
                                                                                                                                                                                                                                                               cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
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96.28;
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: Sequence 3, Application US/07864004B

: Patent No. 5364771
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APPLICANT: LOllar, John S.
APPLICANT: Runge, Marschall S.
APPLICANT RUNGE, Hybrid Hun
                                                                                    Query Match
Best Local Similarity
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[NFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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MEDLIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 MOLECCE NO
ANTI-SENSE: NO
ANTI-SENSE: NO
TYPE: N-terminal
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
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                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: |
ORIGINAL SOURCE:
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                  372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 F
CITY: Atlanta
107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/0
FTILING DATE: 07 APRIL 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 9009 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature (Domain Structure) LOCATION: 5001 7053,
                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                    58.9%;
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/note= "Equivalent to the A3-C1-C2 domain",
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                                                                                    Score 589; DB 1;
Pred. No. 1.1e-175;
                                                                        Mismatches
                                                                                                      DB 1;
                                                                                                      Length 9009;
                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08251937A Patent No. 5583209
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 10
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILLING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 31-MAY-1994
                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 tgggtqcagtqgaactgtcatgggactatatgcaaagtgatctcgggtgagctgctgtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       912 tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                      CITY: Atlanta
                                                                                                                                                                                                                                                                   STREET:
REFERENCE/DOCKET NUMBER:
                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                      MEDIUM TYPE:
                                                                                                                                                                                                                             COUNTRY:
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              REGISTRATION NUMBER:
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                                                                                                                                                                                    Floppy disk
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            29,476
    EMU106DIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 604; Conservative
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INFORMATION FOR SEQ ID NO: 3:
                                            912
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LOCATION: 5001 . 7053
OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
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                                                                                                                                                  AAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAAGAAGATGATA 586
                                                                                                                                                                       CACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGA 526
                                                                                                                                                                                                                                                   cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga
TGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAAG
                  tggcctctgacccactgtgctttacctactcatatctttctcatgtggacctggtaaaag 971
                                                                        AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA 646
                                                                                                                                                                                                                                                                                                       CCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTA 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 589; DB 1;
Pred. No. 1.1e-175;
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Matches 604; Conservative Best Local Similarity

58.9%; 96.0%;

Score 589; DB 1; Pred. No. 1.1e-175;

Length 9009; Indels

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Gaps

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Mismatches

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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-212-133A-1
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                         FEATURE:
                                                                                                                                                                                                                                            TISSUE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: March 1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                 NAME/KEY:
LOCATION:
                                                                                                       OTHER INFORMATION:
                                                                                                                    NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 . . . 2277
                                                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                        NAME/KEY: misc_feature (Domain Structure) LOCATION: 5125 7053
                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   707 ACTTGAATTCAGGCCTCATTGGAGCCCTA 735
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                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/864,004 FILING DATE: 07-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Georgia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08212133A
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100 Peachtree Street
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                  /note=
VIII."
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domain"
                                                                                                    /note=
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                                                                                                    "Equivalent to the A1-A2 domain."
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                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                APPLICANT: Emory University
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                            COMPUTER: TEM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
          ATTORNEY/AGENT INFORMATION:
NAME: Pratt, John S.
REGISTRATION NUMBER: 29,476
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COUNTRY:
                                                    APPLICATION NUMBER: FILING DATE: 07-JUN CLASSIFICATION: 435
                                                                                                                                                                                                                           CITY: Atlanta
                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                       ADDRESSEE:
REFERENCE/DOCKET NUMBER:
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Y: US
                                                                                                                                                                                                                                           1100 Peachtree Street,
                                                                                                               PatentIn Release #1.0,
                                                                                                                                                                                                                                                         Kilpatrick & Cody
                                                              IUMBER: US/08/474,503
07-JUN-1995
 EMU106CIP(3)
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OTHER INFORMATION: OTHER INFORMATION: VOTHER INFORMATION: VUS-08-474-503-1
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Best Local
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ORIGINAL SOURCE:

^^^^NTSM: Homo sapien
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LENGTH: 9009 base pairs
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LOCATION:
912 tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
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                              AAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAA
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VIII."
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Pred. No. 1.1e-175;
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US-08-670-707A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
GONG base pairs
                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Home
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/US94/13200
                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-MAR-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 15-NOV-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lollar, John S. TITLE OF INVENTION: Hybrid Human/Animal Factor VIII NUMBER OF SEQUENCES: 40
                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                              OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                   OTHER INFORMATION: /product= "Domain Structure" OTHER INFORMATION: /note= "Equivalent to the A3-C1-C2 domain"
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         LOCATION:
                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 5125..7053
                                                                                                                                                                                                                                                       TISSUE TYPE:
                         NAME/KEY:
                                                                                                  LOCATION:
                                                                                                                         NAME/KEY:
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REGISTRATION NUMBER: 27,8
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SYSTEM: PC-DOS/MS-DOS
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                                                              /note=
                                                                                /product= "Domain Structure"
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                                                          "Equivalent to the A1-A2 domain"
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Best Local Similarity
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                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                                                                                                                                      APPLICANT: Lollar, John S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612 aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               552 acgcaagatttcctcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432 ccacctgcttcttctgtgccttttgcgattctgctttagtgccaccagaagatactacc
                                                                            ZIP: 80303
                                                                                                                STATE: Colorado
                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
                                                                                          COUNTRY:
                                                                                                                                 CITY: Boulder
                                                                                                                                                   ADDRESSEE: Greenlee, Winner and Sullivan, P.C STREET: 5370 Manhattan Circle Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtcatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatggtccaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctactgga 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGCTTCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAAAAGAAGATGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAGACTCTGTTTGTAGAATTCACGGTTCACCTTTTCAACATCGCTAAGCCAAGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGTGTACA
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 compatible
PC-DOS/MS-DOS
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96.0%;
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/note= "cDNA encoding human factorVIII"
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586 851

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491 166

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526 851

791

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OTHER INFORMATION: /product= "Domain"
OTHER INFORMATION: /note= "cDNA encod
US-09-037-601-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/037,601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/864,004 FILING DATE: 07-APR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                   612
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                                                                                                                                                                                                                                                                                 372 actgacatccactttttctttttctccacaggtatcgatccaccatgcaaatagagctct 431
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                                                                                                                                                                                                                                                               107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
                                                                                                                        227
                                                                                                                                                          492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature LOCATION: 1..2277
OTHER INFORMATION: /pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 11-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: WO POSTILLING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ferber, Donna M
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                           CCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTTTAGTGCCACCAGAAGATACTACC 226
aaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaaggccac
                                                                      acgcaagatttccttcctagagtgccaaaatcttttccattcaacacctcagtcgtgtaca 611
                                                                                                                                       tgggtgcagtggaactgtcatgggactatatgcaaagtgatctcggtgagctgcctgtgg
                                                                                                                      TGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGG
                                                                                                                                                                                                                                                                                                                                     604;
                                                    ACGCAAGATTTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGTGTACA
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5125..7053
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                                                                                                                                                                                                                                                                                                                                                    58:98;
96.08;
                                                                                                                                                                                                                                                                                                                                                                                                                   note- "cDNA encoding human factorVIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Domain Structure"
/note= "Equivalent to the A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Domain Structure"
/note= "Equivalent to the Al-A2 domain"
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                                                                                                                                                                                                                                                                                                                                  Score 589; DB 4; 1
Pred. No. 1.1e-175;
0; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Equivalent to the A3-C1-C2 domain"
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PCT-US93-03275-3
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                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER.
                FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: EM
                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 07-APR-
                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lollar, John S. APPLICANT: Runge, Marschall S.
                                                  ANTI-SENSE: NO
                                                               HYPOTHETICAL:
                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  347 AAAAGACTCTGTTTGTAGAATTCACGGTTCACCTTTTCAACATCGCTAAGCCAAGGCCAC 406
                                                                                                                                     TYPE: NUCLEIC ACID
                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 19930
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 |
CITY: Atlanta
 ORGANISM:
                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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Homo sapien
                                                                                                      linear
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; NAME/KEY: misc_feature
; LOCATION: 1.2277
; OTHER INFORMATION: /note= "Domain Structure:
; OTHER INFORMATION: Equivalent to the Al-A2 domain"
PCT-US93-03275-3
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE: Liver
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5001..7053
OTHER INFORMATION: /note= "Domain Structure:
OTHER INFORMATION: Equivalent to the A3-C1-C2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
467
                                                                                                                                                                                          407
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                                                                                                                                                                                                                                                                                                                                                                                   107 ATTAACCTTTTGCTTCTCCAGTTGAACATTTGTAGCAATAAGTCATGCAAATAGAGCTCT 166
                                                                                                                                                  CCTGGATGGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTA 466
                                                                                                                                                                                                   cctggatgggtctgctaggtkctaccatccaggctgaggtttatgatacagtggtcatta 731
                                    tggcctctgacccactgtgccttacctactcatatctttctcatgtggacctggtaaaag
                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%; Score 589; DB 5; Length 9009; 96.0%; Pred. No. 1.1e-175; rative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                       971
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Search completed: January $\stackrel{4}{\cdot}$ 8, 2002, 17:23:52 Job time: 12483 sec

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OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      323.4
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Copyright (c) 1993 - 2000 Compugen Ltd.
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1006
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AI225600
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2366.192 Million cell updates/sec
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AK014835 Mus muscu
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BF150467 uy86b07.y
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17542	0402	38492	15667	13898	97689	26533	56867	28692	12269	15843	28333	4401	F38378	G97562	3528	I19566	BE308999	1451	I42854	53253	87358	14466	91737	37152	10771	13839	3657	17258	91601	1454	183	5326
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ALIGNMENTS

REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM RESULT BG477974 FEATURES COMMENT VERSION ACCESSION DEFINITION Locus TITLE JOURNAL source Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 954)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) BG477974 954 bp mRNA EST 21-MAR-2001 602522966F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4641352 5', BG477974 CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1408 row: c column: 17 High quality sequence stop: 626. Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/CTD/DTP Unpublished (1999) BG477974.1 GI:13410253 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4641352" /clone_lib="NIH_MGC_20" /tissue_type="melanotic melanoma" /lab_host="DH10B (phage-resistant)"

AL556703

BE912296

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RESULT 2
AA817854/c
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ORGANISM
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacat-atgtctggcaggtcctg---aaagagaatggtccaatggcctctgacccactg- 928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tgatcagaccagtcaaa--gggagaaagaagatgata-aagtcttccctggtggaagcca
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Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                     ceruloplasmin mRNA, complete AA817854 AA817854.1 GI:4198380
                                                                                                                                                                                                                                                                                                                                     discovery
                                                             Normalization and subtraction: two approaches
                                                                                       Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Ròdentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                       Rattus
                                                                                                                                                                                                                               Norway
                                                                                                             (bases 1 to 456)
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Pred. No. 1.5e-83;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                         cds, mRNA sequence
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  AI526753
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The sequence tag present in the cDNA between the NotI site and the
oligo-dT track served to identify it as a clone from the normalized
adult Ovary library. cDNA Library Preparation: M. Fatima Bonaldo,
Ph.D. Clone distribution: clones will be available through Research
Genetics This clone is also available through the I.M.A.G.E.
Consortium at LLNL (info@image.llnl.gov). IMAGE ID-1767329
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451 Eckstein Medical Research Building Towa
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYA-No
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/note="Vector: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_I: Not I; Site_2: Eco RI; This library
consists of a mixture of individually tagged normalized
libraries constructed from rat placenta, adult lung, brain
, liver, kidney, heart, spleen, ovary, and muscle. The tag
is a string of 3-5 nucleotides present between the Not I
site and the oligo-dT track which allows identification of
the library of origin of a clone within the mixture."

a 105 c 101 g 144 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="UI-R-A0-ae-g-10-0-UI"
/clone_lib="UI-R-A0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Sprague-Dawley"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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55.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

Waterston,R. and Wilson,R.

The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MarratM/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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AI526753
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xref="taxon:10090"
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/sex="female"
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288 CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM10912 row: j column:
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                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                       /note="organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH" a 131 c 148 g 177 t
                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma'
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="FVB/N"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10972 row: g 'column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procuremed: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 783)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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BG977142
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                                        Conservative
                                                                                                                                               Site_2: Not1; Cloned unidirectionally. Prim
Library constructed by Life Technologies. In
providing Samples: Jeffrey Green, M.D., NIH"
a 161 c 176 g 210 t
                                                                                                                                                                                                                                                       /clone_lib="NCI_CGAP_Mam6"
/sex="female, Virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:4977442"
                                                                                                                                                                                                                                                                                                                                                                                             /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                     'note="Organ; 'mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                                                      9.98;
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Pred. No. 9e-18;
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The RIF
                                                                                                    Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer casearch. 10 (11), 1757-1771 (2000)
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AK014835.1
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Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning Methods in enzymology. 303, 19-44 (1999)
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Adachi,J., Alzawa, K., Akahira,S., Akimura,T., Aono,H., Arai,A., Adachi,J., Alzawa,K., Akahira,S., Fukudishi,Y., Furuno,M., Arakawa,T., Carninci,P., Fukuda,S., Fukudishi,Y., Furuno,M., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shibata,X., Shibata,Y., Shibata,Y., Shibata,Y., Tayawa,A., Shiraki,T., Sanaka,T., Tejima,Y., Tayawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y., Toya,T., Yasunishi,A., Yoshida,X., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
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5 (bases 1 to 3739)
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768 c 821 g
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/db_xref="MGD:MGI:88476"
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="testis"
/clone_lib="RIKEN_full-length enriched mouse cDNA library"
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI225600 1006 bp mRNA EST 29-OCT-1998 uj06c05.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1891112 5' similar to gb:M13699 CERULOPLASMIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1006)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washu-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMAN);, mRNA sequence.
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                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality sequence stop: 463.
                                           Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                        ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI show be used to isolate the cDNA insert. Size selection was
                                                                                                                          performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Sugano mouse liver mlia"
/sex="female"
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                                                                                                                                                                                                                                                                                was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
                                                                                                                                                                                                                                                                                                                                 /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:1891112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="C57BL"
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                             10 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  608 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 667
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                                                                                                                                                                   Seq p
                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                             MGI:1427189
                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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BF150467
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uy86b07.y1
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                              primer: -40RP from Gibco
quality sequence stop: 428.
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/clone="IMAGE:3666421"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
                                                                  /strain=¶C57/B6"
/db_xref="taxon:10090"
                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3666421 5' SW:CERU_MOUSE Q61147 CERULOPLASMIN PRECURSOR ;, mRNA
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Pred. No. 1.3e-17;
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                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM10828 row: k column: 19
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                             Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG862595 632 bp mRNA
602795978F1 NIH_CGAP_Mam4 Mus
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Clone distribution: MCC clone distribution information can
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
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                                                                                                                                                                                                                                                                                                                                                                                         AA865338
                                                                                                                                                                                                                                                                                                                            sequence.
                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   AA865338.1
Tissue Procurement: Christopher Moskaluk, M.D.,
                                                          Unpublished (1997) -
                                                                                     Tumor Gene Index
                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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/organism="Mus musculus"
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cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

cDNA Sequencing by: Washington University Genome Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 www-bio.llnl.gov/bbrp/image/image.html
                                                                                                  BE912296 878 bp mRNA EST 29-SEP-2000 601666013F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:3966051 5',
                                           BE912296.1 GI:10409387
                                                               BE912296
                                                                                   mRNA sequence.
  house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NCI_CGAP_Kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
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Pred. No. 5.2e-17;
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LOCUS AL556703 918 bp mRNA EST 16-FEB-200:
DEFINITION AL556703 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK005Y102
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                                                                                                                                                                                                                                                                                                                                               361 ACCAAGGAGTATGAGGGAGCCGTCTACCCTGACACACCACTGATTTTCAACGGGCTGAT 420
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                                                                                                                     538 AAAGATATTGCATCAGGACTCATAGGA 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TATAAGAAGGCCCTTTATTTTGAGTACACAGATGGCACCTTTAGTAAGACTATAGACAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 608 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 667
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                                                                                                                                                                                                                                                                   GACAAAGTGCTTCCCGGACAACAGTATGTGTATGTGCTGCATGCC---AATGAGCCAAGT 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                   attacacttaagaacatggcttcccatcctgtcagtcttcatgctgtttggtgtatcctac 787
                                                                                                                                                                                           CCTGGAGAGGGAGACAGCAATTGTGTGACCAGGATTTACCACTCCCATGTTGATGCTCCA 537
                                                                                                                                                                                                                             ccaatggcctctgacccatgtgccttacctactcatatctttctcatgtggacctggta 967
                                                                                                                                                                                                                                                                                             gataaagtetteeetggtggaageeataeatatgtetggeaggteetgaaagagaaatggt 907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGCCTGGCTAGGGTTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT 300
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
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188 c 195 g 227 t
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/db_xref="taxon:10090"
/clone="IMAGE:3966051"
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/tlssue_type=""tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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AV653260
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966 taaaagacttgaattcaggcctcattggagcccta 1000
                                                                                                                                  559 CAAAAGATATTGCCTCAGGACTCATCGGACCTTTA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 TATATAAGAAGGCCCTTTATCTTCAGTACACAGATGAAACCTTTAGGACAACTATAGAAA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 AACCGGTCTGGGTTTTTTAGGCCCCTATTATCAAAGCTGAAACTGGAGATAAAGTTT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  666 ggccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtgg 725
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                                                                                                                                                                                                                                   GTCCTGGGGAAGGAGATGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC 558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr,
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/clone_lib="LTI_NFLO06_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; lst strand cDNA
/note="Vector: pCMVSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
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169 c 192 g 253 t
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52.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgtacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaa 665
                                                                                                                                                                                                                                 atgataaagtcttccctggtggaagccatacatatgtctggcaggtcctgaaagagaatg 905
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                                                                                                     taaaagacttgaattcaggcctcattggagcccta 1000
                                                                                                                                          GTCCTGGGGAAGGATGGCAATTGTGTGACTAGGATTTACCATTCCCACATTGATGCTC
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                                                                                                                                                                                                                                                                                                                207;
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Henno sapiens CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genqme Center at Shanghai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: hanzg@chgc.sh.cn
This clone is available at CHGC in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; 1 (bases 1 to 634)
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Similarity 52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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/clone_lib="GLC"
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/dev_stage="Adult"
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Pred. No. 1.6e-16;
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728 attacacttaagaacatggcttcccatcctgtcagtcttcatgctgttggtgtatcctac 787
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                                                                                                                                                                                                                                                                                                                                         Local Similarity
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GTTCACTTAAAGAACCTTGCCTCTAGGATCTACACTTTTCATGCACATGGGGTAACGTAC
                                                                                                                                   ccaccctggatgggtctgctaggtcctaccatccaggctgaggtttatgatacagtggtc
                                                                                                       CCAGCCTGGCTAGGGTTTTTAGGCCCCTGTCATCAAAGCTGAAGTTGAAGATAAAGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA461838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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608 tacaaaaagactctgtttgtagaattcacggatcaccttttcaacatcgctaagccaagg 667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 576)
NIH-MGC http://mgc.ngi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: LLAM9137 row: 1 column: High quality sequence stop: 576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
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Clone distribution: MGC clone distribution information can
Cound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                             178
                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                     /note="Ogan: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: WptI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Glibert Smith, NIH"

119 c 127 g 151 t 1 others
                                                                                                                                                                                                                                                                                                                                                            /clone_ib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
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/strain="FVB/N"
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Search completed: January 8, 2002, 15:13:44 Job time: 4820 sec

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SUMMARIES

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ALIGNMENTS

ORIGIN	BASE COUNT		source	FEATURES	JOURNAL		TITLE	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AR138378	RESULT 1
	1375 a 1151 c 1155 g 1318 t	/organism="unknown"		Location/Qualitiers	Patent: US 6200560-A 14 13-MAR-2001;	target cells	Adeno-associated virus vectors for expression of factor viii by	Couto, L.B., Colosi, P.C. and Qian, X.	1 (bases 1 to 4999)	Unclassified.	Unknown.	Unknown.		AR138378.1 GI:14480723	AR138378	Sequence 14 from patent US 6200560.	AR138378 4999 bp DNA PAT 10-5001-2001	1	

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Guery Match 100.0%; Score 1000; DB 6; Length 4999; Best Local Similarity 110.0%; Pred. No. 1.2e-299; Indels 0; Gaps 1 garcaagtgateigttggcoccaatgattattcaccygcatcaagacccaaggatgaccygattlates 10; Indels 0; Gaps 1 garcaagtgateigttggcoccaatgattattcaccygcatcaagacccaaggatgaccygattlateigtgaal 120 20 GANCAAGTGCTCCACCCTCAAAGTTATCACCACAATGATTATCACAAAGTCTCAAGACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACTTATCACCAAACATATTAT
atch 100.0%; Score 1000; DB 6; Length 4999; 1000; Conservative 0, Mismatches 0; Indels 0; Gaps gatcasgitygatcigtiggcaccaatgattattcacggcatcasgagcaccaggitygatcigcacgidillillillillillillillillillillillillil

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1 (bases 1 to 4999)
Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated vectors for expression of factor VIII by target cells
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tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                    GGATTCATCTGGGATAAAACACAATATTTTAACCCTCCAATTATTGCTCGATACATCCG
                                                                                              ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
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                                          TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA
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AR138377
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Couto,L.B., Colosi,P.C. and Qian,X.
Adeno-associated virus vectors for
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                        al Similarity
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Sequence 13 from patent US
AR146887
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Couto,L.B., Colosi,P.C. and Qian,X.
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            ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga
                                                                                                        CCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAGGCACAGGA
                                                                                                                                                                                                                    GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
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Seed, B. and Haas, J.
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1 1072 c 1036 g
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tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                               tactgcttcatcotactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
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                                                                                               GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
                                                                                                            gcaagtggacttccagaagacaatgaaagtcaccaggagtaactactcaggggagtaaaatc 540
                                                                                                                                                                                                                                                TTTAAATAGTTGCAGCATÖCCATTGGGAATGGAGAGTAAAGCAATATCAGATGCACAGAT
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                                                              tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 600
                                                  TCTGCTTACCAGCATGTATGTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCA
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99.4%; Pred. No. 2.7e-234;
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GGATTCATCTGGGATAAAACACAATATTTTTAACCCTCCAATTATTGCTCGATACATCCG 4470
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                                                            tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                              TACTGCTTCATCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGACT 4650
                                                                                                        tactgcttcatccttactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
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                                               TCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAATCCAAAAGAGTGGCT
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Sequence
AR071306
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Voorberg, J.J.
Hybrid proteins with
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tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact
                              tttaaatagttgcagcatgccattgggaátggagagtaaagcaatatcagatgcacagat
                                                                     tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                                             GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT 4410
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Voorberg, J.J.
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Sequence 1 from patent US
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Location/Qualifiers
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tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
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                           GGATTCATCTGGGATAAAACACAATATTTTTAACCCTCCAATTATTGCTCGATACATCCG
                                          ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT
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177105
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Yonemura, H., Tajima, Y., Sugawara, K. and Masuda, K.
Process for preparing human coagulation factor VIII protein complex
Patent: US 5693499-A 1 02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown
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                                                 tcagaagttctccagcctctacatctctcagttttatcatcatgtatagtcttgatgggaa 120
TCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATCATGTATAGTCTTGATGGGAA 6386
                                                                                                                                                                                                                                                                                                                                             Sequence 1 from patent:US. 127063
                                                                                                                                                                                                                                1 (bases 1 to 7056) pittman,D., Rehemtulla,A., Wozney,J.M. and Chimeric procoagulant proteins patent: US 5563045-A 1 08-OCT-1996;
                                                                                                                                                                                                                                                                                Unclassified.
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                                                    1 (bases 1 to 7272)
Sarver, N. and Drohan, W.
Factor VIII-C analogs
Patent: EP 0265778-Al 3 04-MAY-1988;
                                                                                                                                                        Sequence 3 from Patent EP 0265778 I05404
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Best Local Si Matches 793; Query Match

Similarity

79.0%;

Score 790; DB 6; Pred. No. 3e-234; Mismatches

DB 6; Length 7272; Indels

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Eukaryota; Metazoa; Chordata; Çraniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to §967)
Saenko,E.L. and Strickland,D.K.
Methods of reducing factor viii clearance and compositions therefor Patent: WO 0071714-A 1 30-NOV-2000;
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Best Local Similarity

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IRWYLLSMGSNENIHSIHFSGHVFTVRRKEEYKMALYNLYPGVFETVEMLPSKAGIWR
VECLIGEHLHAGMSTLEFLYVSNKCOTPLGMASGHIRDFGITASGGYGGMAPKLARLHY
SGSINAWSTKEPFSWIKVDLLAPMIIHGIKTQGARQKESSLYISQFIIMYSLDGKKWQ
TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
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EVEDNIMVTFRNQASRPYSFYSSLISYEEDQRQGAEPRKNFVKPNETKTYFWKVQHHM
APTKDEFDCKAWAYFSDVDLEKDVHSGLIGPLLVCHTNTLNPAHGRQVTVQEFALFFT
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FKKKDTILSLNACESNHAIAAINEGONKPEIEVTWAKOGRTERLCSONPPVLKRHORE
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VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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171409
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Retroviral delivery of full length factor VIII
Patent: US 5681746-A 1 28-OCT-1997;
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Nature 312 (5992),
85061548
Data kindly reviewe
                                       Wood, W.I., Capon, D.J., Simonsen, C.C., Eaton, D.L., Gitschier, Keyt, B., Seeburg, P.H., Smith, D.H., Hollingshed, P., Wion, K.I. Delwart, E., Tuddenham, E.G.D., Vehar, G.A. and Lawn, R.M. Expression of active human factor VIII from recombinant DNA
                                                                                                                                                                                Human mRNA for X01179
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110. .166
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DSFTPYVNSLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQDLY"
167. .7162
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/db_xref="taxon:9606
<1..109
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1898 c 1833 g
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7163" .8967
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TYRGNSTGTLMVFFGNVDSSGIKHNIFNPPIIARYIRLHPTHYSIRSTLRMELMGCDL
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QHDGMEAYVKVDSCPEEPQLRMKNNEEAEDYDDDLTDSEMDVVRFDDDNSPSFIQIRS
VAKKHPKTWVHYIAAEEEDWDYAPLVLAPDDRSYKSQYLNNGPQRIGRKYKKVRFWAY
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VVITLKNMASHPVSLHAVGVSYWKASEGAEYDDQTSQREKEDDKVFPGGSHTYVWQVL
KENGPMASDPLCLTYSYLSHVDLVKDLNSGLIGALLVCREGSLAKEKTQTLHKFILLF
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110. .7165
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1. .8967
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99.4%;
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Pred. No. 3.1e-234;
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                                Unclassified.

1 (bases 1 to 9009)

Lollar, J.S. and Runge, M.S.

Hybrid human/animal factor VIII

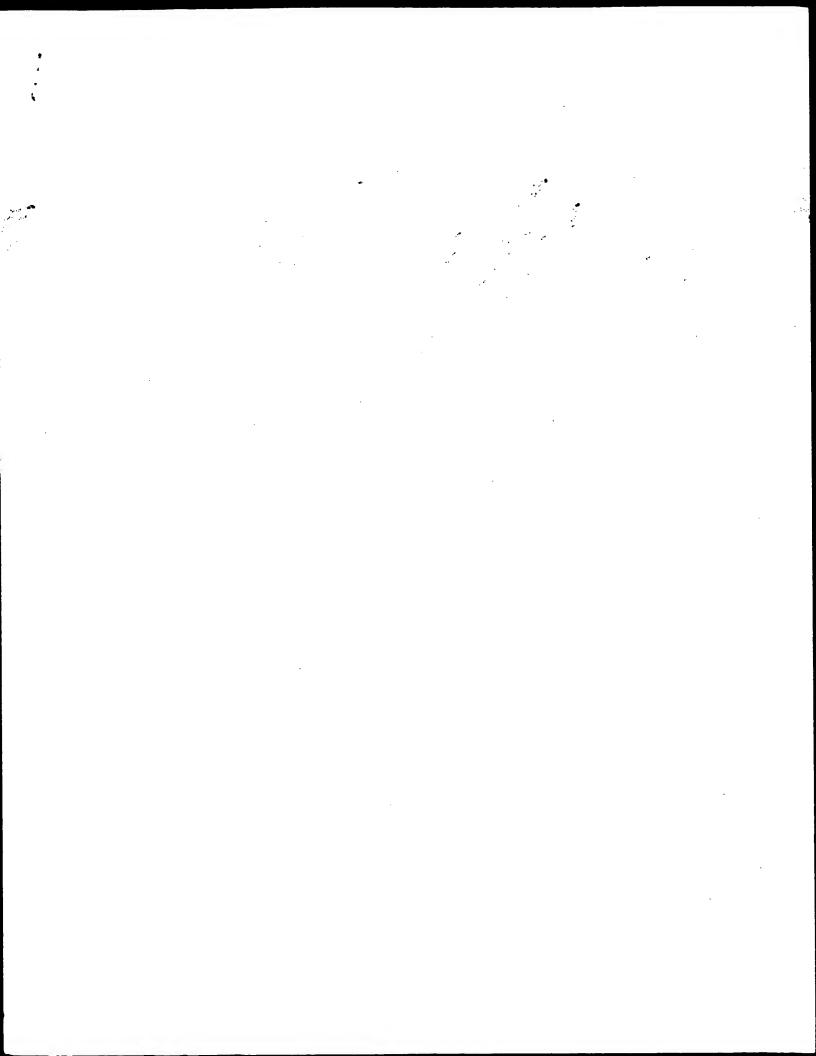
Patent: US 5744446-A 1 28-APR-1998;

Location/Qualifiers
                                                                                                                                                               AR003710 9009 bp DNA
Sequence 1 from patent US 5744446
AR003710
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Search completed: January 8, 2002, 17:27:05 Job time: 12716 sec



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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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ALIGNMENTS

AAD00122

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AAD00122 standard; DNA; 4999 BP.

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20-OCT-1998;
24-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                          Recombinant Adeno Associated Vector; rAAV; pVm4.1cF8deltaB; promoter; human Factor VIII; hFVIII; EF1alpha; human elongation factor-lalpha; human growth hormone; hGH; ITR; inverted terminal repeat; haemophilla;
                                                                                                                                                                                                                                                                                       Recombinant adeno associated vector construct, pVm4.1cF8deltaB
                                                                                                                                                                                                                                                                                                                31-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                       AAD00122;
                                                                                                                                                                                                                                gene therapy; ds.
                                                                                                                                                                                     WO200023116-A1.
                                                                                                                                        19-OCT-1999;
                                                                                                                                                                                                           Adeno associated virus.
New recombinant adenovirus-associated vector, useful for gene therapy
                        WPI; 2000-339536/29.
                                                                   (AVIG-) AVIGEN INC.
                                              Couto LB, Colosi PC;
                                                                                           98US-0104994.
99US-0125974.
99US-0364862.
                                                                                                                                          99WO-US24495.
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to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence - \,
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Example 9; Fig 6; 92pp; English

CC (rAAV) construct pVm4.1cPBdeltaB. This expression vector comprises the Crawly construct pVm4.1cPBdeltaB. This expression vector comprises the CC promoter, first intron (-573 to +985) of human elongation factor-lalpha CC (EFlalpha) gene, human Factor VIII coding sequence (hGH). This sequence is polyadenylation signal from human growth hormone (hGH). This sequence is first 57 bp encoding the 19 amino acid signal peptide, Al and A2 domains can satisfy a mino acids signal peptide, Al and A2 domains can segment comprises the N-terminus of the B domain. The light chain cC and 5 amino acids from the N-terminus of the B domain and the A3. CC and C2 domains. Both the heavy and light chain segments are cloned cC into the same plasmid seperated by 42 nucleotides coding for 14 residues control sequences, that directs the transcription and translation of the C factor VIII gene. The adeno-associated viral vectors are used for gene control treat haemophilia. This method allows prolonged expression of the therapy, because of their broad host range, safety profile and duration XX

Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other:

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                                               tetgettaccageatgtatgtgaaggagtteeteateteeageagteaagatggeeatea
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Conservative
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useful in gene therapy for treating haemophilia

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RESULT
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The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is
                                                                                                                 Claim 19; Fig 6; 90pp; English.
                                                                                                                                                      Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood
                                                                                                                                                 coagulation factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric - Adeno associated virus.
Chimeric - Homo sapiens.
Chimeric - Unidentified.
                                                                                                                                                                                                             WPI; 2001-417955/44.
                                                                                                                                                                                                                                                                        (AVIG-) AVIGEN INC.
                                                                                                                                                                                                                                                                                                    22-DEC-1999; 99US-0470618
                                                                                                                                                                                                                                                                                                                                 21-DEC-2000; 2000WO-US34925
                                                                                                                                                                                                                                                                                                                                                                                             WO200145510-A1.
                                                                                                                                                                                                                                                                                                                                                                 28-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pVm4.lcF8-B; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    blood clotting disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human factor VIII expressing rAAV vector pVm4.1cF8-B partial sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4999 BP; 1375 A; 1151 C; 1155 G; 1318 T; 0 other;
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                                                                                                    4720 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgaggcacagga 4779
                                   661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720
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                                                    781 cctctactgactcgagcctaataaaggaaatttatttcattgcaatagtgtgttggttt 840
841 tttgtgtgcggccgcaggaacccctagtgatggagttggccactccctctctgcgcgctc 900
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Sequence 11933 BP; 3258 A; 2818 C; 2717 G;

3140 T; 0 other;

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                              CC and polyadenylation signal from human growth hormone (hGH). This sequence is inserted between the AAV inverted terminal repeat (ITR) regions. The CC first 57 bp encoding the la mino acid signal peptide, Al and A2 domains CC express the comprises the heavy chain gene segment with the CC and 5 amino acids from the N-terminus of the B domain. The light chain CC alone comprises the C-terminal 85 amino acids of B domain and the A3, CC express the beavy and light chain segments are cloned CC and C2 domains. Both the heavy and light chain segments are cloned CC into the same plasmid seperated by 42 nucleotides coding for 14 residues of the B domain, that is deleted. This plasmid is operably linked to CC of the B domain, that directs the transcription and translation of the CC control sequences, that directs the transcription are used for gene CC therapy to treat haemophilia. This method allows prolonged expression of therapy, because of their broad host range, safety profile and duration CC of expression in the infected hosts.
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24-MAR-1999;
30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hFVIII; HNF-3 albumin promoter; human elongation factor-lalpha; Erlalpha; human growth hormone; hGH; inverted terminal repeat; ITR; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant adeno associated vector construct, pAAV-F8-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Adeno Associated Vector; rAAV; pAAV-F8-1; human Factor VIII;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200023116-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adeno associated virus
                                                                                                                                                                                                                                                                                                              The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-f8-1. This expression vector comprises the HNF-3 albumin promoter, the first intron (-573 to +985) of human elongation factor-laipha (BFlalpha) gene, human Factor VIII coding sequence (hFVIII) factor-laipha (BFlalpha) gene, human Factor VIII coding sequence (hFVIII)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant adenovirus-associated vector, useful for gene therapy to treat hemophilia, comprises at least a portion of factor VIII operably linked to control sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Couto LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AVIG-) AVIGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-339536/29.
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4930 cctcagtgagcgagcgcgcgcagctgcctgcaggacat 4969
                                                                               4870 gctcgctcactgaggccgggcgaccaaaggtcgcccgacgcccgggctttgcccgggcgg
                                                                                                                                                                    4810 thtgtgtgcggcaggaacccctagtgatggagttggccactccctctctgcgcgctc 4869
                                                                                                                                                                                                                                                        4755 cctctactgactcgagaataaaagatcagagctctagagat-----ctgtgtgttggttt 4809
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                                                                                                    901 gctcgctcactgaggccgggtgaccaaaggtcgcccgacgcccgggctttgcccgggcgg 960
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121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180

3975 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 4034

1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60

Matches Query Match

979;

Conservative

Local Similarity

95.4%; Score 954.4; DB 22; Length 11933; 97.9%; Pred. No. 1.7e-287;

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16;

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AAD08612
Sequence 11933 BP; 3258 A; 2818 C; 2717 G; 3140 T; 0 other;
                                  backbone. It comprises HNF-3.mouse albumin promoter, a synthetic intron based on human elongation factor lalpha (EPlalpha) and immunoglobulin G (IGG) intron sequences, B-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both the light and heavy chains of human factor VIII.
                                                                                                                                   second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is useful in gene therapy for treating haemophilia A in mammals, in particular humans. The rAAV vector provides high level and long term expression of biologically active clotting factor VIII in vivo. The present sequence is paAV-FB-1 vector without the plasmid
                                                                                                                                                                                                                                            administering a recombinant adeno-associated virion (rAAV) comprising a nucleotide sequence encoding the light chain of factor VIII and a
                                                                                                                                                                                                                                                                                  The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises
                                                                                                                                                                                                                                                                                                                                               Claim 18; Fig 5; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Treating blood clotting disorder, especially hemophilia in mammals, by administering recombinant adeno-associated vectors which express blood
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Chimeric - Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
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                                                        Plasmid DL26 encoding human B-domain deleted factor VIII.
                 coagulation disorder; ss.
                             Adeno-associated virus vector; B-domain; factor VIII; haemophilia A;
                                                                                       29-JUN-2001
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                                                                                                                                    vector. The vector comprises a heterologous nucleotide sequence encoding B-domain deleted factor VIII operably linked with at least one enhancer and at least one promoter. The method results in the production of high titer rAAV vector stocks carrying the B-domain deleted factor VIII transgenes and expression cassettes, which generate adequate titers of virus for in vivo administration. The recombinant vectors are useful for treating haemophilia A, where the liver expresses the encoded B-domain deleted factor VIII, which is secreted into the blood. They are also useful for the treatment of other coagulation disorders. The present sequence encodes a B-domain deleted factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200127303-A1.
                                                                                                                                                                                                                                                                                                                                                  New recombinant adeno-associated virus vector, useful for treating haemophilia A, comprises heterologous nucleotide sequence encoding B-domain deleted human factor VIII operably linked with liver-preferred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2000; 2000WO-US28221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYNC-) UNIV NORTH CAROLINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-1999;
                                                                                                                                                                                                                                                                              The specification describes a recombinant adeno-associated virus (rAAV)
                                                                                                                                                                                                                                                                                                           Claim 64; Fig 1; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-273781/28.
                                                                                                                                                                                                                                                                                                                                      expression control element -
                                                                                                            Sequence 7944 BP; 2142 A; 1902 C; 1909 G; 1991 T; 0 other;
                                                       Local Similarity
1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
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/note= "hepatitis B virus EnhI enhancer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "inverted terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4916..5084
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/note= "TK polyA sequence"
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/note= "human B-domain deleted factor VIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150..278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "inverted terminal repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420..4835
                                                            87.1%;
92.7%;
                                                0;
                                                            Score 870.8;
Pred. No. 1.8
                                                 Mismatches
                                                                1.8e-261;
                                                                              DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stepan AM,
                                                      Indels
                                                                              Length 7944;
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                                                      21; Gaps
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AAN90654
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Homo sapiens.
                                                Human Factor VIII:C;
                                                                        DNA encoding 740 Arg-1649 Glu human Factor VIII:C.
                                                                                                                                                         AAN90654;
                                  naemophilia A.
                                                                                                                     26-JUN-1990
                                                                                                                                                                                  AAN90654 standard; DNA; 4275 BP.
                                                                                                                                                                                                                                                                               5006
                                                                                                                                                                                                                                                                                                                                                4946
                                                                                                                                                                                                                                                                                                                                                                                           4886 gcacgggtgttgggtcgtttgttcggatccagatctaggaacccctagtgatggagttgg 4945
                                                                                                                                                                                                                                                                                4646 gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt
                                                                                                                                                                                                                                                                                                                                                                                                               820 attgcaatagtgttgtttgttttttgtgtgcggccgcaggaacccctagtgatggagttgg 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4346 trtaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 gtggactctcttttttcagaatggcaaagtaaaggtttttcaggggaaatcaagactcctt 660
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                                                                                                                                                                                                                                                                                                                          999cgacctttggtcgcccggcctcagtgagcgagcgagcgcgcag 5051
                                                                                                                                                                                                                                                                                                                                                                                                                                                            cctctactgactcgagcgagttcttctgaggggatcggcaataaaaagacagaataaaac 4885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | CCagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgagggacagga 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
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                                                                                                                 (first entry)
                                    Ad.RE.neo; 740 Arg-1649 Glu Factor VIII:C;
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QΥ
                            Matches 790;
                                                                                                                      When translated, Arg-740 of the carboxyl terminus of the H chain is directly bonded by a peptide bond to Glu-1649 of the amino terminus of L chain. It is used to transform animal cells so that they produce The expression vector is plasmid Ad.RE.neo. The expression vector has at least one promoter upstream of AAN90654. The transformants can constantly and continuously produce human Factor VIII:C in high yield on a commercial scale. The human Factor VIII:C so intact Factor VIII:C money and continuously produce human factor viiii: The formation in the human blood plasma. It is useful
                                                                                    Sequence 4275 BP; 1245 A; 941 C; 945 G; 1144 T; 0 other
                                                                                                                for treating haemophilia A patients.
                                                                                                                                                                                                                                                                                                          Prodn. of recombinant human Factor-VIII-C using animal cells transformed with a vector contg. the gene for {\sf var}
                                                                                                                                                                                                                                                                        Fig 1(1) - 1(13); ; 32pp; English.
                                                                                                                                                                                                                                                                                                  Factor VIII:C and a promoter
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                                                                                                                                                                                                                                                                                                                                                                                                   Sugiyama T, Masuda K,
                                                                                                                                                                                                                                                                                                                                                                                                                            (KAGA ) CHEMO-SERO-THERAP (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                          1989-078467/11.
                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88EP-0114769
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1..4275
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    100.0%; Prea. ....
100.0%; Prea. ....
                               79.0%; Score 790; DB 10; 100.0%; Pred. No. 2.4e-236;
                                                                                                                                                                                                                                                                                                                                                                                                   Tajima Y,
                                                                                                                                                                                                                                                                                                                                                                                                 Yonemura
                    0;
                                            Length 4275;
                   Indels
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              Gaps
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                                        3846 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 3905
                                                                                                                        3786 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat
                                                                                                                                                                                                          3726 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                                                                                                                                                                                                                                                 3666
                                                                                                                                                                                                                                                                                                                                                                             3606 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 3665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3546 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa
421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                            361 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3486
                                                                                                                                                                                                                               241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
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                                                                                                                                                                                                                                                                                                                                                                                                      121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180
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                                                                                                                                                tttaaatagrtgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 360
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Length 4629;

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RESULT
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                                                                                                                                                                                                                                         07-JUN-1995;
10-JUN-1993;
25-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX88293 standard; DNA; 4629 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Factor VIII with B domain deleted cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX88293;
                                                                                                                                                                                                                                                                                                                                               US5935935-A.
                                                                                                                                                                                                                                                                                                                                                                                             Adenoviral vector; Factor VIII; Factor IX; clotting factor; treatment; haemostatic; haemophilia \hat{A}; haemophilia B; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    781 cctctactga 790
                                                                                                                                                                                                                                                                                                                    10-AUG-1999
                                                                                                                                                                                                                                                                                             07-JUN-1995;
                                   This invention describes movel adenoviral vectors comprising at least one DNA sequence encoding a clotting factor (Factor IX or Factor VIII). The vectors of the invention have haemostatic activity. The vectors are useful for the treatment of hemophilia A or hemophilia B by gene therapy. This sequence represents human Factor VIII cDNA which has the B domain
                                                                                                                                                                                          Connelly S,
                                                                                                                                                                                                                (GENE-) GENETIC THERAPY INC
                                                                                                                                                                  WPI; 1999-457617/38.
                                                                                                               Example 1; Column 53-58; 90pp; English.
                                                                                                                                      Adenoviral vectors useful for treating hemophilia
 Sequence 4629 BP; 1319 A; 1050 C; 1015 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga
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                                                                                                                                                                                             Kaleko M,
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93US-0074920. .
94US-0218335.
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                                                                                                                                                                                                Smith T;
             1245 T; 0 other
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AAV23339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                481
                                                                                                                                                                                                                                                                               4287 cacacetgtggtgaactetetagacecacegttactgaetegetacettegaatteacee 4346
                                                                                                                                                                              4407
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                                                                                                                                                                                                                                                                                                                                            601 gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 660
                                                                                                                                                                                                                                                                                                                                                                                              541 tetgettaceageatgtatgtgaaggagtteeteateteeageagteaagatggeeatea 600
                                                                                                             AAV23339 standard; DNA; 4670 BP
                                  Human Factor-VIII gene lacking central B domain.
                                                                                      AAV23339;
                                                                                                                                                                                                                                         721 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgagggcacagga 780
         Factor-VIII; blood clotting; human; synthetic gene; codon usage;
                                                             17-AUG-1998
                                                                                                                                                                                                    781 cctctactgactcgagcc 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 3746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 3806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 3866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tttaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat 3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                    gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 4106
                                                                                                                                                                                                                                                                                                                                   gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 4286
                                                                                                                                                                                                                                                                                             cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
                                                                                                                                                                            cctctactgagggtggcc 4424
                                                                                                                                                                                                                             ccagagttgggtgcaccagattgccctgaggatggaggttctgggctgcgaggcacagga 4406
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                                                                (first entry)
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99.4%;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 790; DB 20;
pred. No. 2.5e-236;
p: Mismatches 5;
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Synthetic.

Homo sapiens.

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                                                                 4013 tactgottoatcot&ctitaccaatatgtttgccacctggtotocttcaaaagctcgaot 4072
                                                                                                                                    3953 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 4012
              421 tcacctccaagggaggagta@tgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                                                                                                                                                                       3893 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                                                                                                                                                                                                        3833 ggattcatctgggatamaacacamtatttttmaccctccamttattgctcgatmcmatccg 3892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This gene codes for a human Factor-VIII protein that lacks the central B domain (amino acids 760-1639) of the native protein. In a novel, claimed synthetic gene (see AAV23288), non-preferred or favored by highly expressed human genes to provide high-level from 29 pairs of Oligonucleotides (see AAV23340-97) which served as AAV23289-91) are used for production of recombinant proteins in mammalian cells at levels of the invention (see also AAV23289-91) are used for production of recombinant proteins in the natural genes. They can also be used in gene therapy.
                                                                                                                                                      301 tttaaatagttgcagcatgccattgggaatggaggtaaagcaatatcagatgcacagat 360
                                                                                                                                                                                                                       241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4670 BP; 1325 A; 1072 C; 1036 G; 1237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            121 gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 180
                                                                                                                                                                                                                                                                                                                                                                                                                       61 tcagaagttctccagcctctacaactctcagtttatcatcatgtatagtcttgatgggaa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New synthetic eukaryotic gene(s) - in which non-preferred or less preferred codon(s) are replaced to provide high level expression mammalian cell(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Loca!
                                                                                   tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
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                                                                                                                                                                                                                                                                                          99attcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 240
                                                                                                                                                                                                                                                                                                                                                                                                           tcagaagttctccagcctctacptctctcagtttatcatcatgtatagtcttgatgggaa 3772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.0%; Score 790; DB 19; 99.4%; Pred. No. 2.5e-236;
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This cDNA encodes the beta-domain deleted SQN deletion protein of human

Example 28; Pages 210-213; 272pp; English.

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AAV19581
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                                                 administered to provide long term systemic expression of therapeutic protein in blood, useful in, e.g. treating hyper-coagulable
                                                                              New replication defective recombinant retro-viruses - which can be
                                                                                                                                                                                                                                                    04-JUN-1997;
03-JUL-1996;
13-AUG-1996;
                                                                                                                        P-PSDB; AAW46246.
                                                                                                                                    WPI; 1998-086966/08.
                                                                                                                                                                               De LA VEGA D,
                                                                                                                                                                                                 Allen JR,
                                                                                                                                                                                                                      (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                    Replication defective; recombinant retrovirus; RRV; therapeutic protein; haemophilia; thrombosis; hypercoagulable disorder; liver disease; human; hepatilis; thalassemia; phenylketonuria; Lesch-Nyhan syndrome; diabetes; cystic fibrosis; Duchenne's Muscular Dystrophy; hypercholesterolemi; hypopituitarism; adenine deaminase deficiency, HIV infection; anaemia; Guacher's syndrome; high blood pressure; Alzheimer's disease, autoimmune; inflammatory disease; factor VIII; ss.
                                                                                                                                                                                                                                                                                                         02-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                WO9800541-A2
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                Lee R,
                                                                                                                                                                                           Barber JR,
                                                                                                                                                      ber JR, Boder M, Chang SMW, Chong K;
Depolonj, Greengard J, Hsu DC, Iban
R, Mittelstaedt DM, Prussak CE, Res
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cc intravenously to a human. The long term systemic expression results in a cc intravenously to a human. The long term systemic expression results in a cc deasurable level of the therapeutic protein being produced in the blood cc of the human for a period of at least 30 days after the administration of cc the RRV vector preparation. RRV's can be used for in vivo delivery of cc therapeutic protein to treat, e.g. haemophilia A, haemophilia B, cc thrombosis, hypercoagulable disorders, liver diseases such as hepatitis, cc disorders such as thalasemia, phenylketonuria, Lesch-Nyhan syndrome, cc disorders such as thalasemia, phenylketonuria, Lesch-Nyhan syndrome, cc diabetes, hypopitutarism, adenine deaminase deficiency, alphal-cc diabetes, hypopitutarism, adenine deaminase deficiency, alphal-cc antitrypsin deficiency, Guacher's syndrome, anaemia, infections such as companied pressure, Alzheimer's disease, autoimmune or cc inflammatory disease or graft versus host disease. RRV's are capable of cc surviving inactivation in human serum thereby allowing efficient gene cc transfer over prolonged periods of time.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressing a therapeutic protein. The RRV preparation is resistant to degradation by human complement and is capable of inducing long term systemic expression of the therapeutic protein when administered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor VIII. This is used in the construction of recombinant retroviral vectors expressing human factor VIII. The invention provides the preparation of replication defective recombinant retrovirus (RRV)
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Sequence 4832 BP; 1381 A; 1089 C; 1055 G; 1307 T; 0 other;

Query Match

Local Similarity

79.0%;

score 790; DB 19; pred: No. 2.6e-236;

DB 19;

Length 4832;

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gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 4315
                                                                               totgottaccagoz#tgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 600
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               gtggactctcttttttcagaatggcaaagttaaaggtttttcagggaaatcaagactcctt 660
                                                               totgottaccagcatgfatgtgaaggagttcctccatctccagcagtcaagatggccatca
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administered to a haemophilia A patient

is resistant

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03-JUL-1996;
13-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       retrovirus; vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9800542-A2
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     expressing a B domain-deleted human Factor VIII protein, where recombinant RV is capable of infecting human cells, is resistan to degradation by human complement and is capable of inducing long-term (at least 30 days and up to 6 months or longer post-injection) systemic expression of Factor VIII when administrated to a harmonician
                                                                           Factor VIII, the SQN deletion does not influence the in vivo pharmacokinetics, but the reduced size of the molecule appears to decrease proteolytic degradation. The invention relates to preparations of replication defective recombinant retrovirus (RV)
                                                                                                                                           deletion mutant SQN (see AAW44372) of human Factor VIII. The SQN mutant is created by fusing Ser-743 to Gln-1638 of native Factor VIII (see AAW44373) to form a Ser-Gln-Asn (SQN) link between the A2
                                                                                                                                                                                                                  Claim 6; Page 174-175; 236pp; English.
                                                                                                                                                                                                                                                                                                    P-PSDB; AAW44372.
                                                                                                                                                                                                                                                                                                                   WPI; 1998-086967/08.
                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
                                                                                                                                  and A3 Factor VIII domains. When compared to plasmid-derived
                                                                                                                                                                                        This DNA sequence includes a coding region for the
                                                                                                                                                                                                                                                       domain-deleted human factor VIII or human factor IX for the
                                                                                                                                                                                                                                                                      New replication defective recombinant retroviruses - which express B
                                                                                                                                                                                                                                          treatment of haemophilia
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                                                                                                                                                                                                                                                                                                                                                       JR,
Vega
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NJ, Greengard J, Hsu DC, Ib
: DM, Prussak CE, Respess JG
                                                                                                                                                                                                                                                                                                                                                              Ibanez CE;
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                                                                                                                                            4436 cctctactgagggtggcc 4453
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                                                                         AAT69811 standard;
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Local Similarity 99.4%; Pr
                                                                                                                                                                                                              ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgaggcacagga 780
                                                                                                                                                                                                                                                         cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
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(first entry)
                                                                          DNA;
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Pred. No. 2.6e;236;
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4411 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                                                                                                                                                                                                                                                                                                        A DNA molecule (AAT69811) codes for Factor VIII-dB695-HCII (AAW18670), a hybrid protein in which amino acids 712-736 of Factor-dB695 (Factor VIII de1868-1562) B-domain are replaced by amino acids 51-80 from the acidic region (and potential thrombin-binding site) of human heparin cofactor II (HCII). It was obtd. by PCR amplification (see also AAT69812-13) of the HCII acidic region from total liver cDNA, fusion to sequences encoding Factor VIII aa706-711 and aa737-743, and incorporation of the construct into plasmid pCLB-dB695. The hybrid protein, which can be expressed using gene therapy techniques, has increased procoagulant activity cowing to the HCII acidic region, and can be used to treat blood coagulation disorders such as haemophilia A.
                                                                                                                                                                                                            4231
                                                                                                                                              4291
                                                                                                                                                                                                                                                                                                                                              Sequence 5035 BP; 1484 A; 1127 C; 1110 G; 1314 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 52-60; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       donor anticoagulant or antithrombotic protein - useful for treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid Factor VIII with modified activity, comprises region from
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                                                                                                                                                                                                               1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
               99attcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                               gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttcttttggcaatgt 180
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                                                            gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt 4410
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                   RESULT 12
AAA49231
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AAA49231 standard; DNA; 5094 BP.
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                                                                                                                               781 cctctactgactcgagcc.798
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Hemostatic; antianemic; antidiabetic; nootropic; neuroprotective; osteopathic; antisickling; immunostimulant; gene therapy; collage; endothelial cell; peripheral blood; buffy coat cell; VEGF; PCR primer; vascular endothelial growth factor; bovine brain extract, haemophilia; Factor VIII; human; transgene; adenosine deaminase deficiency; ss; sickle cell anaemia; thalassemia; diabetes; alpha-antitrypsin deficiency; slickle cell anaemia; brain disease; heart disease; immune system defect;
                                                                                                                                                                                                                                                                                                                        DNA construct HSQ/eGFP for transforming endothelial cells.
                                                                                                                                                                                                                                                                                                                                                           26-SEP-2000 (first entry)
                                                                                                                                                                         Homo sapiens.
(MINU ) UNIV MINNESOTA.
(UYEM-) UNIV EMORY.
(HEBB/) HEBBEL R P.
                                                                                      24-NOV-1999;
                                                                                                                  08-JUN-2000
                                                                                                                                             WO200032750-A1
                                                         24-NOV-1998;
                                                                                                                                                                                                   tracture; osteoporosis
                                                     98US-0109687.
                                                                                     99WO-US28033.
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Recondition relates to a method for expanding the population of CC endothelial cells (BC) obtained from peripheral blood, by culturing, CC in contact with a collagen I coated surface, buffy coat cells obtained CC in contact with a collagen I coated surface, buffy coat cells obtained CC in containing vascular endothelial growth factor (VEGF) and free of bovine CC containing vascular endothelial growth factor (VEGF) and free of bovine CC protein extract. EC are useful for treating hemophilia by introducing it CC from the blood stream of a mammal, so that an effective amount of CC protein extract is secreted in the blood stream of the mammal. CC Phis sequence represents a huamn factor VIII gene into which an CC enhanced green fluorescent protein coding sequence has been inserted. CC protein (eGFF); the last painto acids of the SQ linker peptide; an enhanced green fluorescent CC clomain extivation peptide; an enhanced green fluorescent CC clomain and the hfVIII C2 domain. Transgenic EC transduced in vitro CC are useful for improving prosthetic implants. EC is also useful for content of the activity of an enzyme. EC is also useful in gene CC deaminase deficiency, sickle cell anemia, thalassemia, hemophilia, CC domainse deficiency, sickle cell anemia, thalassemia, hemophilia, CC transition base and the variety of diseases including adenosaine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expanding population of endothelial cells useful to biocompatibilize implantable medical devices comprises contacting buffy coat cells with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 19; Fig 3; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endothelial growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen I coated surface in culture medium comprising vascular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (LINY/) LIN Y
                                                  repairing bone fractures and to treat or prevent osteoporosis.
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Query Match

Local Similarity

100.0%;

79.0%; Score 790; DB 21; 100.0%; Pred. No. 2.7e-23

.7e-236;

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Gaps

Length 5094; Indels

Sequence 5094 BP; 1435 A; 1207 C; 1169 G; 1283 T; 0 other;

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RESULT 13
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                                Disclosure; Page 27-36; 61pp; English.
                                                                    Nucleic acid encoding porcine factor VIII - use porcine and human porcine *chimerfc factor VIII
                                                                                                                                           Kaufman RJ, Pittman D, Rehemtulla A,
                                                                                                                P-PSDB; AAR55352.
                                                                                                                                                                              (GEMY ) GENETICS INST INC
                                                                                                                                                                                                        13-NOV-1992;
14-SEP-1993;
                                                                                                                                                                                                                                               01-OCT-1993;
                                                                                                                                                                                                                                                                         26-MAY-1994.
                                                                                                                                                                                                                                                                                                   W09411503-A
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                             Factor VIII; haemostasis; haemophilia A; clotting cascade; fibrinogen; fibrin; thrombin; proteolytic enzyme; co-factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of human factor VIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ66615 standard; cDNA; 7056 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ66615;
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                                                                                                                            1994-183504/22.
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93US-0121202
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                                                                                                                                                Wozney JM;

    used to obtain

                                                                  for treating
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US Patent No. 4,757,006 issued July 12, 1988 and in Toole et al.,

Prepn. of human factor VIII cDNA has been set forth in detail, e.g.,

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Best Local
                                                                                                                                                                                                                                                           6807
721 ccagagttgggtgcaccagattgccctgaggatggaggttctgggggtgcgggggcacagga 780
                                                                                         661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                include those where various domains of the human factor VIII have been replaced, in whole or in part, by analogous porcine factor VIII domains, and include, chimeric forms where the Al and/or A2 domains, in whole or in part, of the human factor VIII sequence have been replaced, in whole or in part, by the Al and/or the A2 domains of porcine factor VIII. Specifically provided are chimeric factor VIII sequences comprising the A1, A2, A3, B, Cl and C2 human domains as other segments, such as the regions corresp. to the AA numbers 336-372, 336-740, 372-740, 700-740 and combinations of these regions have been replaced in whole or in part with porcine factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6327 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 6386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6267 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 6326
                                                                                                                                                                                                                                                                                                                                                                                                                                          421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 312:312(1984). A recombinant clone contg. the nucleotide sequence in AAO66615, designated as pSP64-VIII, is on deposit at the ATTC under Accession No. ATCC 39812. Chimeric forms of factor VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VIII sequences as set forth in AAQ66616 and AAR55353.
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                                                                cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc
                                                                                                                                                                           gtggactctctttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt 660
                                                                                                                                                                                                                                       tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca
                                                                                                                                                                                                                                                                  tctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca
                                                                                                                                                    gtggactctctttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt
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Pred. No. 3.2e-236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 7056;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-SEP-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AAW00465), a trace plasma glycoprotein which acts as a cofactor in conjunction with Factor-IXa in the activation of Factor-X. Retroviral vectors comprising the full-length cDNA can be efficiently packaged into infectious retroviral particles. These may be used to the conjunction of the conjunctio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A full-length cDNA clone (AAT31031), codes for human Factor-VIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retroviral vector directing expression of full length factor VIII used in the gene therapy and treatment of haemophilia A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAW00465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-DEC-1995;
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                                                                                                                                                                                                                                                                                                             Sequence 8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                         transduce cells either in vivo or ex vivo. Factor-VIII expressed from such transduced cells will be processed and transported in a fashion analogous to the expression product of a normal Factor-VIII gene. Retroviral particles harbouring such vectors will be useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 58-68; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON VIAGENE INC
                             61
                                                                                                                                                                                                              Local Similarity
                                                                                                       1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
                                                                                                                                                                                                                                                                                                                                                                the gene therapy of haemophilia A.
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                           tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
                                                                           gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 6435
Conservative
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                                                                                                                                         receptor-dependent clearance; receptor-independent clearance; haemophilia; half-life; ss.
                                                                                                                                                                        Factor VIII; human; A2 domain; C2 domain; LRP-mediated plasma clearance;
                                                                                                                                                                                                                 Human factor VIII cDNA, SEQ ID NO:1.
                                                                                                                                                                                                                                                     13-MAR-2001 (first entry)
24-MAY-2000; 2000WO-US14111.
                                     30-NOV-2000
                                                                       WO200071714-A2
                                                                                                       Homo sapiens.
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24-MAY-1999;

99US-0135847

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Claim 41; Page 86-101; 121pp; English.
                                                                                                                                               Factor VIII mutants having increased half-life useful for treating hemophilia, comprise one or more amino acid substitutions in the A2 and/or C2 domain of factor VIII
                                                                                                                                                                          P-PSDB; AAB48843.
                                                                                                                                                                                                         (AMNA-) AMERICAN NAT RED CROSS
                                                                                                                                                                                2001-025163/03
                                                                                                                                                                                            Strickland
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The invention relates to human factor VIII mutants comprising an amino CC acid substitution at one or more positions in the A2 domain and/or an CC amino acid substitution at one or more positions in the C2 domain. CC The invention also encompasses a factor VIII mutant which lacks a B CC domain (AAB48842). The factor VIII mutants have an increased half-life CC in the bloodstream. The A2 domain mutants exhibit reduced LRP-dependent CC (receptor-dependent) clearance of factor VIII, while C2 domain mutants can be compassed to the compassed half-life CC have reduced receptor-independent clearance. The invention also relates CC to a method of using RAP (receptor associated protein), a protein which compassed the half-life of factor VIII. The mutant CC internalisation, to increase the half-life of factor VIII. The mutant CC factor VIII proteins, and nucleotides encoding them, are useful composed to a composition of the composition of the composition of the invention section of the invention. The invention with a mutant factor VIII protein or DNA of CC the invention. The invention provides means of increasing the half-life CC of factor VIII by reducing its clearance from plasma. The present content of the composition sequence represents cDNA encoding human factor VIII

Sequence 8967 BP; 2841 A; 1898 C; 1833 G; 2395 T; 0 other;

Score 790; DB 22; Length 8967; Pred. No. 3.6e-236;

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Best Local Similarity 99.2%;
Matches 793; Conservative
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                             tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
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cctctactgagggtggcc
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Search completed: January Job time: 12996 sec 8, 2002, 17:33:36

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	12	c 11	10	c 9	8	7	6	5	4	ω	2	_	Result No.
	193.2	193.4	194	201.4	217.4	280.4	350.8	398.8	446.4	449.2	506	573.8	Score
	19.3	19.3	19.4	20.1	21.7	28.0	35.1	39.9	44.6	44.9	50.6	57.4	Query Match 1
di	247	384	265	444	401.	639	515	• 482	943	815	720	692	Query Match Length DB
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ALIGNMENTS

RESULT

source	FEATURES		AUTHORS TITLE JOURNAL COMMENT	SOURCE ORGANISM	BG700655 LOCUS DEFINITION ACCESSION VERSION
/Organism="Homo sapiens" /db_xref="taxon:9606" /dlone="IMAGE:4815208" /clone_1ib="NIH_MGC_95" /tissue_type="hippocampus"	http://image.llnl.gov Plate: LLAM10711 row: o column: 17 High quality sequence stop: 690. Location/Qualifiers	Tissue Procurement: Miklos Palkovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Frail: Cranbs-ranail nih.gov	EST. human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 692)	BG700655 692 bp mRNA EST 07-MAY-2001 602682272F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4815208 5', mRNA sequence. BG700655 BG700655.1 GI:13970214

ORIGIN

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RESULT
AL601022
                       KEYWORDS
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                     720 bp mrNA

NDKFZp313G1439_r1 313 (synonym: hl.

DKFZp313G1439 5', mRNA sequence.

AL601022

AL601022.1 GI:15164528

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99.3%;
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Pred. No. 2.
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                                                                                    14-AUG-2001
                                                                      clone
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GGCTGCGAGGCACAGGACCTCTACTGA
                                     ggctgcgaggcacaggacctctactga 790
                                                                                            tacettegaattcacccccagagttgggtgcaccagattgccctgaggatggaggttctg
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                                                                       TACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTTCTG
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Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No s1 sequence available. This clone (DKFZp31301439) is available at the RZPD in Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST (Duesterhoeft, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duesterhoeft, A., Lauber, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pTriplEx2; Site_1: SfiIA; Site_2:
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="DKFZp313G1439"
/clone_lib="313 (synonym: hlcc2)"
/dev_stage="adult"
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/db_xref="taxon:9606"
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Pred. No. 2.4e-138;
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clone@rzpd.de.
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 452
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                                521
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
ATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAA 271
                                                                                                                                                                                                                                                          atggagttgatgggctgtgatttaaatagttgcagcatgccattgggaatggagagtaaa 340
                                                                                                                                                                                                                                                                                                       ATTATTGCTCGATACATCCGTTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGC 211
                                                                           aataatocaaaagagtggctgcaagtggacttccagaagacaatgaaagtcacaggagta 520
                                                            AATAATCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genomics@hri.co.jp
HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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1 (bases 1 to 815)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 81-438-52-3952
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/note="Vector: pME18SFL3
207 c. 204 g 19
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/clone_lib="PLACE1"
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90.3%; Pre
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PLACE1001786 5', mRNA
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Best Local Similarity
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                 583 cagtcaagatggccatcagtggactctcttttttcagaatggcaaagtaaaggtttttca
242 CAGTCAAGATGGCCATCAGTGGACTCTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCA
                                                                                                                                                                                                                                                                                       taatccaaaagagtggctgcaagtggacttccagaagacaatgaaagtcacaggagtaac 522
                                                                                         tactcagggagtaaaatctctgcttaccagcatgtatgtgaaggagttcctcatctccag 582
                                                                                                                                               TAATCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAAC
                                                                        TACTCAGGGAGTAAAATCTCTGCTTACCAGCATGTATGTGAAGGAGTTCCTCATCTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 943)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B (T1 phage-resistant)"
note="organ: brain; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 2.3 kb. Constructed by Life
Technologies..Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:4915634"
/clone_lib="NCI_CGAP_Brn67"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="anaplastic oligodendroglioma with 1p/19q
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Pred. No. 1.1e-120;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20892-9643, USA
Tel: 301 443 170
Fax: 301 443 989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: M.B. Soares Lab Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, N
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Mammalia; Eutheria; Rodentia; Sciurognathi; Murldae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
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301 443 9890
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normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amyddala, basal ganglia, pineal gland, striatum, hipoccampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1, clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
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                                                                                                                                                                                                                                                                                                                                                                                 /clone="UI-M-BH3-asm-g-04-0-UI"

/clone_lib="NIH_BMAP_M_S4"

/clone_lib="NIH_BMAP_M_S4"

/dev_stage="27-32 days"

/lab_host="DH10B (Life Technologies)"

/lab_host="DH10B (Life Technologies)"

/note="Vector: pT7T3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I: Site_2: Eco RI: The

NIH_BMAP_M_S4 library is a subtracted library of a series,

ultimately derived from a mixture of individually tagged

normalized libraries from ten regions of the mouse brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 CAATGGTTGCAAGTGGACTTACAAAAGACAATGAAAGTCACTGGAATAATAACCCCAGGGA
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                      ,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Han,Z., Chen,Z., Hu,R. and Chen,J. Homo saplens NPC library cDNA clones Unpublished (2000) Contact: Qinghua Zhang
                                                                                                                                                                                                                                                                             AV748467 NPC Homo sapiens cDNA clone NPCAXA05
AV748467
AV748467.1 GI:10906315
                                                                                                                       Song, H., Peng, Y., Gu, Y., Yang, Y. Qian, B., Liu, F., Qu, J., Gao, X.,
Contact: Qinghua Zhang
Shanghai Institute of Endocrinology, Rui-Jin Hospital
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 Rui-Jin II Road, Shanghai 200025, P. R. China Tel: 86-21-64370045(ex.663332)
Fax: 86-21-64743206
Email: mbshi@ms.stn.sh.cn
  chicken.
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                  BI067808 639 bp mRNA. EST 15-JUN-2001 pg4fin.pk008.h22 normalized chitken fat cDNA library Gallus gallus cDNA clone pgfin.pk008.h22 5' similar to gi|6679733 ref|NP_032003.1| coagulation factor VIII; Factor VIII [Mus musculus splQ06194[FA8_MOUSE COAGULATION FACTOR VIII PRECURSOR PACCOAGULANT COMPONENT) pir[A47004 coagulation factor VIII precursor couse gb|AAA37385.1| (L05573) coagulati, mRNA sequence.
Phasianinae; Gallus.
                                                                                                                 BI067808.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pituitary"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agcattcgcagcactcttcgcatggagttgatgggctgtgatttaaaatagttgcagcatg 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCAACACCACCAGTACACAGATGATGTTCTTTGCAAACGTGGACGCAACCACGGTGAAA 66
                                                                                                                                                                                                                                                                            acaatgaaagtcacaggagtaactactcagggagtaaaatctctgcttaccagcatgtat 559
                                                                                                                                                                                                                                                                                                              AATGCATGGAGACCAGAGACCAACAGCCCCAGTGAGTGGGTTGCAGGTTGGACTTTGAAGCA 366
                                                                                                                                                                                                                                                                                                                                                                             TCCAATATCTTCTCCAGCTGGTCACCCTCCCAGGCCCGCCTGAACCTGCAGGGAAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCTTAGGAATGGAGAGCAAAGGGATCCCTGACCAGCGCATCTCTGCATCATCCTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCATCCGCACCACACTGCGCATGGAGCTCATTGGCTGCGATCTGAACAGCTGCTCCATG
                                                                                      ctagacccaccgttactgactcgctaccttcgaattcacccccagagttgggtgcaccag
                                                                                                                        AACGGCAAGGAGAAGATTTTCAGGGCAAACAGAGATTACACCAGCACAGTGCTGAACAGC
                                                                                                                                         aatggcaaagtaaaggtttttcagggaaatcaagactccttcacacctgtggtgaactct 679
                                                                                                                                                                                                                                                 ATTGCCCTGNNGNTAGAGTNNNNNNNCTGNNA
                          attgccctgaggatggaggttctgggctgcga 771
                                                           CTGGAGCCNNCGCTCTTTGCCCCGCTATGTGAGGATACATCCCCGCCCACTGGCACAACCAC
                                                                                                                                                                                      GTGAAGGAGTTTGCTGTCTCCAGCAGCCAGGATGGTGTCCACTGGAGCCGGGTCCTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Delaware Townsend Hall, Newark, DE 19717, Tel: 302-831-135 Fax: 302-831-2822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 639)
Cogburn,L.A., Morgan,R.W. and Burnside,J.
Chicken ESTs from fat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cogburn@udel.edu, www
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="fat"
/lab_host="E.coli EMDH10B"
/note="Vector: pSPORT1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="pgfln.pk008.h22"
/clone_lib="normalized chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www.chickest.udel.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
   638
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                             740 attgccctgaggatggaggttctggggttgcgagggcacaggacctctactga 790
                                                                                                                                                                                                                                                                                                                                                                                    620 aatggcaaagtaaaggtttttcagggaaatcaagactccttcacacctgtggtgaactct 679
242 ATTGCTCTGAGGCTTGAGATTCTAGGATGTGAGGCCCAGCAGCAATACTGA 292
                                                                                                                                                         182 CTAGACCCACCATTACTGACTCGCTATCTTCGAATTCACCCCCAGATCTGGGAGCACCAA
                                                                                                                                                                                                                                                                                                                  122 AATGGCAAGGTAAAGGTTTTTCAGGGGAATCAGGACTCATCCACACCTATGATGAATTCT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                560 gtgaaggagttcctcatctccagcagtcaagatggccatcagtggactctcttttttcag 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 acaatgaaagtcacaggagtaactcacgggagtaaaatctctgcttaccagcatgtat 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GTGAAAGAGTTCCTTATTTCCAGCAGTCAAGATGGCCATCACTGGACTCAAATTTTATAC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ACAATGAAAGTCACTGGAATAATAACCCAGGGAGTGAAATCTCTCTTTTACCAGCATGTTT 61
                                                                                                                                                                                                          ctagacccaccgttactgactcgctaccttcgaattcacccccagagttgggtgcaccag 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , complete (MOUSE);, mRNA sequence. {\tt BE847128}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE847128 401 bp mRNA EST 26-SEP-2000 uw22b11.yl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3417405 5' similar to gb:L05573 Mus domesticus coagulation factor VIII mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    //ADE host="Dilion"
//ADE host="Dilion"
//ADE host="Telion"
//ADE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Spleen"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:3417405"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares mouse 3NbMS"
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84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POLYA=Yes.
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                                                                                                                                                                                     nipocoampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, and NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.1, NIH_B
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/lab_host="DHIOB (Life Technologies)"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified
/note:-pt/T3D-Pac (Pharmacia) with a modified
/note:-pt/T3D-Pac (Pharmacia) with a modified
/note:-pt/T3D-Pac (Pharmacia) with a modif
                                                                           was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
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/dev_stage="27-32 days"
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245; Conservative
                                                                                                                                                                                                                                                                                Contact: Marra N/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lc Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mt93e12.rl Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:637486 5' similar to gbxL05573 Mus domesticus coagulation factor VIII mRNA , complete (MOUSE); mRNA sequence.
AA184901 AA184901.1 GI:1168759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 265)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubus,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA184901
                                                                                                                                                                                                               Email: mouseest@Watson.wustl.edu
This clone is available royalty free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                               MGI:389478
                                                                                                                                                                                        IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         house mouse.
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TAG_TISSUE=brain-stems
TAG_SEQ=TCATG"
                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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                                  FEATURES
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                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  375 actttaccaatatgtttgccacctggtctccttcaaaagctcgacttcacctccaaggga 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 agaagacaatgaaagtcacaggagtaactactcagggagtaaaaatctctgcttaccagca 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACTTCACCAACATGTTTGCTACTTGGTCTCCTTCACAAGCTCGACTTCACCTCCAGGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTTTGTGAAAGAGTTCCTTATTTCCAGCAGTCAAGATGGCCATCACTGGACTCAAATTT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgtatgtgaaggagttcctcatctccagcagtcaagatggccatcagtggactctctttt 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGACAATGAAAGTCACTGGAATAATAACCCCAGGGAGTGAAATCTCTCTTTACCAGCA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGACTAATGCCTGGCGACCTCAGGTGAATGATCCAAAACAATGGTTGCAAGT-GACTTAC 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggagtaatgcctggagacctcaggtgaataatccaaaagagtggctgcaagtggacttcc 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATACAATGGCAAGGTAAAGGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226;
                                                                                                        Unpublished (1997)
Other_ESTs: uw22bl1.yl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 384)
                                                                                                                                                                                                                                                                                                                                                                                                                         BE852200 384 bp mRNA EST 26-5EF-2000 uw22b11.x1 Soares mouse 3NbMS Mus musculus cDNA clone IMAGE:3417405 inilar to SW:FA8_MOUSE Q06194 COAGULATION FACTOR VIII PRECURSOR
                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                  BE852200.1 GI:10310464
                                                                                                                                                                                                                                                                                                                             house mouse.
                                                     MGI:1093217
                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:637486"
/clone_lib="Soares mouse 3NbMS"
/organism="Mus musculus
                                ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 194; DB 10;
Pred. No. 2.5e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 265;
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/strain="C57BL/6J"

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REFERENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agactccttcacacctgtggtgaactctctagacccaccgttactgactcgctaccttcg 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGAAATCTCTCTTTACCAGCATGTTTGTGAAAGAGTTCCTTATTTCCAGCAGTCAAGA 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agtaaaatctctgcttaccagcatgtatgtgaaggagttcctcatctccagcagtcaaga 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggcacaggacctctactga 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTCACCCCAGATCTGGGAGCACCAAATTGCTCTGAGGCTTGAGATTCTAGGATGTGA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGCCATCACTGGACTCAAATTTTATACAATGGCAAGGTAAAGGTTTTTCAGGGGAATCA 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tggccatcagtggactctctttttcagaatggcaaagtaaaggtttttcagggaaatca 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218;
                                                                                                                                                                                                1 (bases 1 to 247)

1 (bases 1 to 247)

Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.M., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G. Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
USDA, ARS, US Me&t. Animal Re PO Box 166, Clay Center, NE Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW446518 247 bp
86227 MARC 1BOV Bos t
AW446518
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW446518.1 GI:6988305
EST.
                                                                                         Contact: Smith TPL
                                                                                                                  21180013
                                                                                                                                                                         Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                        Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecòra; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                         libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
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                                                                                                                                  Res. 11 (4),
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3 c 91 g 110 t
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/dev_stage="4 weeks"
/lab_host="DH10B"
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/clone="IMAGE:3417405"
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84.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                     Bos.
                                                                                                                                  626-630 (2001)
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Pred. No. 4.2e-46;
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                                                                Research Center
                                           68933-0166, USA
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                                                                                                                                                                                                                                                                                                                                                      Pecora; Bovoidea;
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Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 TTTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 tcagggaaatcaagactccttcacacctgtggtgaactctctagacccaccgttactgac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGGGAAATCAAGACTCCTTCACCCCCGTGGTGAATGCTCTAGACCCCCCGCTGTTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 97044477
                                                                                                                                                                                                                                                                                                                                     AW456831 431 bp mRNA EST UI-M-BH3-aqw-h-12-0-UI.S1 NIH_BMAP_M_S4 Mus UI-M-BH3-aqw-h-12-0-UI 3', mRNA sequence.
               20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                  20892-9643,
                                                                                                   Contact: Chin, H
                                                                                                                                                                                1 (bases 1 to 431)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                          EST
                                                                                                                                                                                                                                                                                                         AW456831
AW456831.1
                                                                6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
                                                                                    National Institute of Mental Health
                                                                                                                                                      discovery
                                                                                                                                                                    Normalization and
                                                                                                                                                                                                                                                                          house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BACKWARD: GTTTTCCCAGTCACGACG
Plate: 48 row: F column: 20
Seq primer: ATTTAGGTGACACTATAG
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PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Single pass sequencing. Bases call v0.980904.e. Vector identified by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                            247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."
68 c 61 g 62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                         GI:7027048
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                                                                                                                                                                  subtraction: two
                                                                                                                                   791-806 (1996)
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Pred. No. 4.2e-46;
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                                                                                                                                                                  approaches
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                                                                                                                                                                                                                                                                                                                                                          musculus
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              567
                                                                                                                                                                                                                                                                                                                                                                                                                 431
                                                                                                                                                                                                           371
                                                    aagtaaaggtttttcagggaaatcaagactccttcacacctgtggtgaactctctagacc 686
                                                                                                                                                                                                                                                     agttcctcatctccagcagtcaagatggccatcagtggactctcttttttcagaatggca 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagtcacaggagtaactactcagggagtaaaatctctgcttaccagcafgtatgtgaagg 566
                                                                                                                                                                                                                                                                                                                                                                                                       AAGTCACTGGAATAATAACCCAGGGAGTGAAATCTCTCTTTACCAGCATGTTTGTGAAAG 372
                                                                                                                                                                                                      AGTTCCTTATTTCCAGCAGTCAAGATGGCCATCACTGGACTCAAATTTTATACAATGGC- 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements. The following repetitive elements were found in this cDNA sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYA=Yes
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-AAGGTTTTTCAGGGGAATCAGGACTCATCCACACCTATGATGAATTCTCTAGACC 258
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/clone_1ib="NNH-IMAP_M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Tech
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCRamplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTS had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=TCATG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAG_LIB=NIH_BMAP_M_S4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH_BMAP_M_S4 library.
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/strain="C57BL/6J"
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82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 190; DB 10; Length 4
Pred. No. 4.5e-45;
0; Mismatches 45; Indels
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                     269 agcactcttcgcatggagttgatgggctgtgatttaaatagttgcagcatgccattggga 328
                                                                                                                                                                                                                             149
242 CCTACCCTTCGATTGGAACTGCAAGGTTGTGAGGTAAATGGATGTTCCACACCCCTGGGT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 TGAGGCTTGAGATTCTAGGATGTGAGGCCCAGCAGCAATACTGA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747 tgaggatggaggttctgggctgcgaggcacaggacctctactga 790
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                                                                                                                                                                                                                                                                     62 GAGTTCTATGTAGCTTACAGTTCCAACCAGATCAACTGGCAGATCTTCAAAGGGAACAGC
                                                                                                                                                                                                                                                                                             89 cagittatcatcatgtatagtcitgatgggaagagtggcagacittatcgagggaaattcc 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                          2 ATAATCACAGGGATCCAGACCCAAGGTGCCAAACACTACCTGAAGTCCTGCTATACCACA 61
                                                                                                              ttaaccctccaattattgctcgatacatccgtttgcacccaactcattatagcattcgc 268
                                                                                                                                                                                                                   actggaaccttaatggtcttctttggcaatgtggattcatctgggataaaacacaatatt 208
                                                                                    TTTGACCCACCTATTGTGGCTAGATATATTAGGATCTCTCCAACTCGAGCCTATAACAGA 241
                                                                                                                                                                           ACAAGGAATGTGATGTATTTAATGGCAATTCAGATGCCTCTACAATAAAAGAGAATCAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="CSODIO67G24"
/clone_lib="LTI_NFL006_PL2"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://fulllength.invitrogen.com"
192 c 182 g 239 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCAACCCCCCAATCATTTCCAGGTTTATCCGTGTCATTCCTAAAACATGGAATCAAAGT 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCATGGTGGACAAGATTTTTGAAGGAAATACTAATACCAAAGGACATGTGAAGAACTTT 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----aaagtaaaggtttttcagggaaatcaagactccttcacaccctgtggtgaactct 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTATACCATCCACTACAGTGAGCAGGGAGTGGAATGGAAACCATACAGGCTGAAATCC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gagttcctcatctccagcagtcaagatggccatcagtggactctcttttttcagaatggc 625
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 745)
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AL577036
AL577036.1 GI:12939773
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: segref@genoscope.cns.fr,
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                                                                          /Clone_lib-"LTI_NFL006_PL2"
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/note="Wector: pCMVSPRT 6; Site_1: NotI; 1st strand cDNA
/note="Wector: pCMVSPRT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMvSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
                         http://fulllength.invitrogen.com" 160 c 158 g 238 t
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/clone="CS0DI082Y022"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web : www.genoscope.cns.fr
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Search completed: January Job time: 4833 sec 8

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1 US-08-366-851A-1
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1 US-08-251-937A-3
1 US-08-474-503-1
1 US-08-670-707A-1
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4 US-09-037-601-1
5 PCT-US93-03275-3
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US-09-364-862-14

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US-08-817-294-41

US-08-882-083-1

US-08-558-107-1

US-09-243-539-1
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US-08-474-503-5
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Sequence 5, Appli	Sequence 5, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 14, Appl	Sequence 14, Appl	Sequence 4, Appli	Sequence 26, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 42, Appl		Sequence 36, Appl	•	Sequence 38, Appl	Sequence 1, Appli

ALIGNMENTS

US-09-470-618-14

RESULT

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: COLOSI, Peter C.
APPLICANT: COLOSI, Peter C.
TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
TITLE OF INVENTION: by Target Cells
FILE REFERENCE: AVigen-04-082
CURRENT APPLICATION NUMBER: US/09/470,618
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 09/364,862
EARLIER FILING DATE: 1999-07-30
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 15
SOFTMARE: Patentin Ver. 2.0 QУ Db QΥ Db QΥ DЬ Qy В FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-470-618-14 Sequence 14, Application US/09470618 Patent No. 6200560SEQ ID NO 14 Matches 1000; Query Match Best Local Similarity TYPE: DNA ORGANISM: Artificial Sequence LENGTH: 4999 4120 4060 4000 121 181 61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120 \vdash gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttctttggcaatgt tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg Conservative 100.0%; 0, Score 1000; Pred. No. 0; Mismatches DΒ 4. 0; Length 4999; Indels Synthetic 0; Gaps 4119 4239 4179 4059 180 60 240 0;

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GENERAL INFORMATION:

APPLICANT: COULO, Linda B.

APPLICANT: COLOSI, Peter C.

TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: BY TARGET TITLE OF INVENTION: CELLS

FILE REFERENCE: AVIGEN-03743

CURRENT APPLICATION NUMBER: US/09/364,862

CURRENT FILING DATE: 1999-07-30

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER APPLICATION NUMBER: 60/104,994
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US-09-364-862-14
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CURRENT APPLICATION NUMBER: US/09/470,618

CURRENT FILING DATE: 1999-12-29

EARLIER APPLICATION NUMBER: 09/364,862

EARLIER FILING DATE: 1999-07-30

EARLIER APPLICATION NUMBER: 60/125,974

EARLIER FILING DATE: 1999-03-24

EARLIER FILING DATE: 1999-03-24

EARLIER APPLICATION NUMBER: 60/104,994

EARLIER FILING DATE: 1999-03-20
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APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
TITLE OF INVENTION: by Target Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
FILE REFERENCE: AVIGEN-03743
CURRENT APPLICATION NUMBER: 1909/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1998-10-20
NUMBER: 0F SED ID NOS: 14
COMMENDER: 05 SED ID NOS: 14
                                                                                                                                                                                                                                                                                                                      SEQ ID NO 13
                                                                                 Matches 979;
                                                                                                                            Query Match
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                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                    Conservative
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97.9%;
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                                                                                                        Score 954.4; DB 4;
Pred. No. 4.3e-310;
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TITLE OF INV
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 INVENTION:
           Connelly, Sheila
Kaleko, Michael
Smith, Theodore
Adenoviral
                                                 Sheila
Vectors
for
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                            3627 GATCAAGGTGGATCTGTTGGCACCAATGATTATTCACGGCATCAAGACCCAGGGTGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 10-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Treatment of Hemophilia NUMBER OF SEQUENCES: 7
                                                                                                                                                                               181 ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg
                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
nes 793; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/218,335 FILING DATE: 25-MAR-1994 APPLICATION NUMBER: 08/074,920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                               1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg
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                                                                                                               tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                 tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 360
                                                                                                                                                                                                                                                                                             tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
                                                                                               TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA
                                TTTAAATAGTTGCAGCATGCCATTGGGAATGGAGTAAAGCAATATCAGATGCACAGAT
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Pred. No. 4.4e-255;
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                                                  INFORMATION FOR SEQ ID NO: 641:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HIGH LEVEL EXPRESSION TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 cacacctgtggtgaactctctagacccaccgttactgactcgctaccttcgaattcaccc 720
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                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
                                SEQUENCE CHARACTERISTICS:
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CITY: E
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette,
COMPUTER: IBM Compatible
                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 20-SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                   NAME: Elbing, Karen L
REGISTRATION NUMBER:
                                                                                                                                                                                                                      APPLICATION NUMBER:
                  LENGTH:
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nucleic acid
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HAAS, JURGEN
                4670 base pairs .
                                                                                    617-428-7045
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ON: 435
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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: C
US-08-717-294-41
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4433 CCTCTACTGAGGGTGGCC 4450
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Local Similarity 99.4%;
                   781
                                                 721 ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgagggcacagga 780
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                                                                                                                                                                GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
                                                                                                                                                                                                                   gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 540
                 cctctactgactcgagcc 798
                                       CCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAGGCACAGGA 4432
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Pred. No. 4.4e-255;
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US-08-882-083-1

Sequence 1, Application US/08882083 Patent No. 5869292 GENERAL INFORMATION:

APPLICANT:

VOORBERG, Johannes J.

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US-08-882-083-1
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REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
4591 TACTGCTTCATCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGACT 4650
                                                               4411 GGATTCATCTGGGATAAAACACAATATTTTTAACCCTCCAATTATTGCTCGATACATCCG
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                                                                                                                                                                                                                                                                                                                                           4291
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                 361 tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                            241
                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                 tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                                                    99attcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 240
                                                                                                                                                                                                                                                                 GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT 4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         793;
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35..5017
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99.48; Pred. No. 4.6e-255;
99.48; Mismatches 5;
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; LOCATION: US-08-558-107-1
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; Sequence 1, Application US/08558107
; Patent No. 5910481
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                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 13-NOV-10-
CLASSIFTON-1
                                             FEATURE:
                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
33.
                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 5035 base pairs
                                                                                                                                                                                           REGISTRATION NUMBER: 33,715
REFERENCE/DOCKET NUMBER: 30,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                              NAME/KEY:
                                                              TOPOLOGY:
                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                              TELEFAX: (202)672-5399
TELEX: 904136
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                                                                                  Sequence 1, Application US/09243539 Patent No. 6130203
                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                            4771
                            TITLE OF INVENTION: HYBRID PROTEINS WITH MODIFIED ACTIVITY NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
                                                               APPLICANT:
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STREET:
                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATCATGTATAGTCTTGATGGGAA 4350
                                                                                                                                                                                                                                    TCTGCTTACCAGCATGTATGTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCA 4830
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                                                                                                                                                                                                                                                                                                                                      totgottaccagcatgtatgtgaaggagttcctcatctccagcagtcaagatggccatca 600
                                                                                                                                                   CCTCTACTGAGGGTGGCC
                                                                                                                                                               cctctactgactcgagcc.798
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 Washington
          3000 K Street, N.W., Suite 500
                                                              VOORBERG, Johannes J
                    Foley & Lardner
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99.4%; Pred. No. 4.6e-255;
ative 0; Mismatches 5;
                                                                                                                                           5; Indels 0;
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/243,539
APPLICATION NUMBER: US/09/243,539
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: ISACSON, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          4231 GATCAAGGTGGATCTGTTGGCACCAATGATTATTCACGGCATCAAGACCCCAGGGTGCCCG 4290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                  481
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Local Similarity 99.4%;
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                                                                                                                                                                                                                                                                                                                                                                                           gaagtggcagacttatcgaggaaattccactggaaccttaatggtcttcttttggcaatgt 180
                                                                                                              tttaaatagttgcagcatgccattgggaatggagagtaaagcaatatcagatgcacagat 360
                                                                                                                                                                                                                                                               tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
                                                                                                                                                                                TTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAAGCAATATCAGATGCACAGAT 4590
gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcaggggagtaaaatc 540
                                                TCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAATCCAAAAGAGTGGCT 4710
                                                                 tcacctccaagggaggagtaatgcctggagacctcaggtgaataatccaaaagagtggct 480
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Pred. No. 4.6e-255;
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LOCATION: 1..6996

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US-08-276-594A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08276594A Patent No. 5693499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                       NFORMATION FOR SEQ ID NO: 1:
                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                      TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/276,594/
FILING DATE: 18-UUL_1994
CLASSIFICATION: 435.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JUS 07/950,191
FILING DATE: 24-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                FEATURE:
                                                                                                                                                                                                                                   FILING DATE: 24-SEP-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                           TELEFAX: 1-
TELEFAX: 904136
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: ...
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN TITLE OF INVENTION: FACTOR VIII PROTEIN COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K St
CITY: Washington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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NAME/KEY: CDS
                            TOPOLOGY:
                                           STRANDEDNESS:
                                                             TYPE:
                                                                                                                                                                                                       NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             781 cctctactgactcgagcc 798
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                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                        6999 base pairs
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3000 K Street, N.₩., Suite 500
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MASUDA, Kenichi
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                              linear
                                           single
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Best Local Similarity
Matches 790; Conserv
6990 CCTCTACTGA 6999
                                            6810 GTGGACTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTT
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RESULT 11 US-08-121-202-1

Sequence 1, Application US/08121202 Patent No. 5563045

GENERAL INFORMATION:
APPLICANT: Pittman
APPLICANT: Rehemt

APPLICANT:

Wozney, John M. Rehemtulla, Pittman, Debra

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CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Meinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5195A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1210 X8574
TELEFAX: (617)876-5851
FILEFAX: (617) 876-5851
SEQUENCE CHARACTERISTICS:
LENGTH: 7056 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 790; Conserva:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
   6627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kaufman, Randal J.
TITLE OF INVENTION: CHIMERIC PROCOAGULANT PROTEINS
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                          181
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CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                        61 tcagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             1 gatcaaggtggatctgttggcaccaatgattattcacggcatcaagacccagggtgcccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                    tttaaatagttgcagcatgctattigggaatggagagtaaagcaatatcagatgcacagat 360
                                                                                                                                                     tttgcacccaactcatdatagcattcgcagcactcttcgcatggagttgatgggctgtga 300
TACTGCTTCATCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAAGCTCGACT
               tactgcttcatcctactttaccaatatgtttgccacctggtctccttcaaaagctcgact 420
                                                                                                                                 TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA 6566
                                                                                                                                                                                                      GGATTCATCTGGGATAAAAACACAATATTTTTAACCCTCCAATTATTGCTCGATACATCCG 6506
                                                                                                                                                                                                                      ggattcatctgggataaaacacaatatttttaaccctccaattattgctcgatacatccg 240
                                                                                                                                                                                                                                                                                                                                        TCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATCATGTATAGTCTTGATGGGAA 6386
                                                                   TTTAAATAGTTGCAGCATGCCATTGGGAATGGAGAGTAAAGCAATATCAGATGCACAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79.0%; score 790; DB 1; Length 7056; 100.0%; Pred. No. 5.8e-255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/121,202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08366851A Patent No. 5681746
                                                                                                                                                       TELEFAX: (619) 452-2616
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366 arrivelling DATE:
CLASSIFTOR:
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 452-1288
                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Chambers, Daniel M.
REGISTRATION NUMBER: 34,5
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hsu, David Chi-Tang
APPLICANT: Chang, Steven
TITLE OF INVENTION: Retroviral Delivery of Full Length Factor VIII
NUMBER OF SEQUENCES: 3
                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 8967 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
                                      FEATURE:
                                                    MOLECULE TYPE:
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CITY: Sa
STATE: C
COUNTRY:
ZIP: 921
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                                                                   TOPOLOGY:
                                                                                     STRANDEDNESS: both
                                                                                                                                                                                       TELEPHONE:
                  NAME/KEY:
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11055 Roselle
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De Polo, Nicolas J.
Hsu, David Chi-Tang
                                                                   unknown
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                                                                                                                 US-07-864-004B-3
                                                                              Sequence 3, Application US/07864004B Patent No. 5364771
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Best Local Similarity
Matches 793; Conserv
                                                                  GENERAL INFORMATION:
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APPLICANT: Loliar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 6
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NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU1
TELECOMMUNICATION INFORMATION:
TELECHONE: 404-815-6508
TELECRAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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HYPOTHETICAL: N
ANTI-SENSE: NO
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LOCATION: 5001 . . . 7053
OTHER INFORMATION: /note= "Equivalent to
OTHER INFORMATION: domain"
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   6657
                                                                                                                                                                                                                  6477 TCAGAAGTTCTCCAGCCTCTACATCTCTCAGTTTATCATCATGTATAGTCTTGATGGGAA
                                                                                                                                                                                                                                                                                      6417 GATCAAGGTGGATCTGTTGGCACCAATGATTATTCACGGCATCAAGACCCAGGGTGCCCG
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CITY: Atlanta
STATE: Georgia
COUNTRY: US
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OTHER INFORMATION: Onote= "Equivalent to the Al-A2
OTHER INFORMATION: domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                  61 toagaagttctccagcctctacatctctcagtttatcatcatgtatagtcttgatgggaa 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 2277
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                                                                      tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
                                                                                                                                            GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT
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99.4%;
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                                                                                                                                                                                                                                                                                                                                                          Score 790; DB 1; pred. No. 6.8e-255;
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lollar, John S.
APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Porcine Factor VIII
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7077
                               TELECOMMUNICATION INFORMATION: TELEPHONE: 404-815-6367
                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                    STATE: G
                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 I
                                                                                NAME: Pratt, John S. REGISTRATION NUMBER: 29,476
                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                          APPLICATION NUMBER: US 07/864,004 FILING DATE: 07-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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HYPOTHETICAL: NO
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LOCATION: 5001 . . 7053
OTHER INFORMATION: /note= "Equivalent to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleion STRANDEDNESS:
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                                                   tetgettaceageatgtatgtgaaggagttecteatetecageagteaagatggeeatea
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           gtggactctcttttttcagaatggcaaagtaaaggtttttcagggaaatcaagactcctt
                                                                                                          GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 790; DB 1; 1
Pred. No. 6.8e-255;
0; Mismatches 5;
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US-08-212-133A-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9009 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC GOMPATIBLE
COMPUTER: IEM PC GOMPATIBLE
COMPUTER: IEM PC GOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
SOFTWARE: Patentin Release #1.0, Vers
APPLICATION NUMBER: US/08/212/133A
FILING DATE: March 11, 1994
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US/07/864,004
FILING DATE: 07-APR-199.2
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMU/76677
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6558
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ORGANISM: Homo sapien
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APPLICANT: Runge, Marschall S.
TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
NUMBER OF SEQUENCES: 12
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APPLICANT:
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CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30303
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                                                                                                                                                                   NAME/KEY: misc_feature (Domain Structure)
LOCATION: 5125 . . . . 7053
OTHER INFORMATION: /note= "Equivalent to
NAME/KEY: Domain LOCATION: 1.2277 OTHER INFORMATION:
                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                  TISSUE TYPE: Liver
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                          OTHER INFORMATION:
                                                                                            NAME/KEY: misc_feature (Domain Structure) LOCATION: 1 . . . 2277
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                                                                          /note= "Equivalent to the
/note= "cDNA encoding human
                                                                                                                                                                   /note= "Equivalent to the
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                                                                          A1-A2 domain."
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Best Local Similarity 99.4%;
Matches 793; Conservative
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                                                                                                                                                                     gtggactctcttttttcagaattggcaaagtaaaggtttttcagggaaatcaagactcctt
                                                                                                                                                                                                                        tetgettaceageatgtatgtgaaggagtteetcateteeageagtcaagatggeeatea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCTACTGAGGGTGGCC
                      cctctactgactcgagcc 798
                                                               ccagagttgggtgcaccagattgccctgaggatggaggttctggggctgcgaggcacagga 780
                                                                                                                                                                                                                                                                        gcaagtggacttccagaagacaatgaaagtcacaggagtaactactcagggagtaaaatc 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tttgcacccaactcattatagcattcgcagcactcttcgcatggagttgatgggctgtga
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                                                    CCAGAGTTGGGTGCACCAGATTGCCCTGAGGATGGAGGTTCTGGGCTGCGAGGCACAGGA
                                                                                                      CACACCTGTGGTGAACTCTCTAGACCCACCGTTACTGACTCGCTACCTTCGAATTCACCC
                                                                                                                                                         GTGGACTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGACTCCTT
                                                                                                                                                                                                          TCTGCTTACCAGCATGTATGTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCA
                                                                                                                                                                                                                                                            GCAAGTGGACTTCCAGAAGACAATGAAAGTCACAGGAGTAACTACTCAGGGAGTAAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTGCACCCAACTCATTATAGCATTCGCAGCACTCTTCGCATGGAGTTGATGGGCTGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAGTGGCAGACTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATGT 6596
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Pred. No. 6.8e-255;
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Search completed: January Job time: 12603 sec

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